

# SUBSTITUTE SEQUENCE LISTING

RECEIVED  
TECH CENTER 1600/2500  
03 FEB 13 PM 2:43

<110> Anderson, John P.  
Basi, Guriqbal  
Doane, Minh Tam  
Frigon, Normand  
John, Varghese  
Power, Michael  
Sinha, Sukanto  
Tatsuno, Gwen  
Tung, Jay  
Wang, Shuwen  
McConlogue, Lisa

<120> Beta-Secretase Enzyme Compositions and  
Methods

<130> 228-US-NEWC1

<140> 09/723,722

<141> 2000-11-28

<150> US 09/501,708

<151> 2000-02-10

<150> 60/119,571

<151> 1999-02-10

<150> 60/139,172

<151> 1999-06-15

<160> 104

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1503

<212> DNA

<213> Homo sapiens

<400> 1

atggcccaag	ccctgcccctg	gctcctgctg	tggatgggcg	cgggagtgct	gcctgcccac	60
ggcaccacgc	acggcatccg	gctgcccctg	cgcagcggcc	tggggggcgc	ccccctgggg	120
ctgcggtgct	cccgggagac	cgacgaagag	cccaggagac	ccggccggag	gggcagcttt	180
gtggagatgg	tggacaacct	gaggggcaag	tcggggcagg	gctactacgt	ggagatgacc	240
gtgggcagcc	ccccgcagac	gctcaacatc	ctggtggata	caggcagcag	taactttgca	300
gtgggtgctg	ccccccaccc	cttcctgcat	cgctactacc	agaggcagct	gtccagcaca	360
taccgggacc	tccggaaggg	tgtgtatgtg	ccctacaccc	agggcaagtg	ggaaggggag	420
ctgggcaccg	acctggtaag	catcccccat	ggccccaacg	tcactgtgct	tgccaacatt	480
gctgccatca	ctgaatcaga	caagttcttc	atcaacggct	ccaactggga	aggcatcctg	540
gggctggcct	atgctgagat	tgccaggcct	gacgactccc	tggagccttt	ctttgactct	600
ctggtaaaagc	agaccacagt	tcccaacctc	ttctccctgc	agctttgtgg	tgttggttcc	660
cccctcaacc	agtctgaagt	gctggcctct	gtcggaggga	gcatgatcat	tggagggtatc	720
gaccactcgc	tgtacacagg	cagtctcttg	tatacaccca	tccggcggga	gtggtattat	780
gaggtgatca	ttgtgctggg	ggagatcaat	ggacaggatc	tgaaaatgga	ctgcaaggag	840
tacaactatg	acaagagcat	tgtggacagt	ggcaccacca	accttcgttt	gcccagaagaa	900
gtgtttgaag	ctgcagtcaa	atccatcaag	gcagcctcct	ccacggagaa	gttccctgat	960
ggtttctggc	taggagagca	gctgggtgtg	tggcaagcag	gcaccacccc	ttggaacatt	1020
ttcccagtc	tctcactcta	cctaattggg	gaggttacca	accagtcctt	ccgcatcacc	1080
atccttccgc	agcaatacct	gcggccagtg	gaagatgtgg	ccacgtccca	agacgactgt	1140

tacaagtttg	ccatctcaca	gtcatccacg	ggcactgtta	tgggagctgt	tatcatggag	1200
ggcttctacg	ttgtctttga	tcgggcccga	aaacgaattg	gctttgctgt	cagcgcttgc	1260
catgtgcacg	atgagttcag	gacggcagcg	gtggaaggcc	cttttgtcac	cttggacatg	1320
gaagactgtg	gctacaacat	tccacagaca	gatgagtcaa	ccctcatgac	catagcctat	1380
gtcatggctg	ccatctgcgc	cctcttcatg	ctgccactct	gcctcatggt	gtgtcagtgg	1440
cgctgcctcc	gctgcctgcg	ccagcagcat	gatgactttg	ctgatgacat	ctccttgctg	1500
aag						1503

<210> 2  
 <211> 501  
 <212> PRT  
 <213> Homo sapiens

<400> 2

Met	Ala	Gln	Ala	Leu	Pro	Trp	Leu	Leu	Leu	Trp	Met	Gly	Ala	Gly	Val
1				5					10					15	
Leu	Pro	Ala	His	Gly	Thr	Gln	His	Gly	Ile	Arg	Leu	Pro	Leu	Arg	Ser
			20					25					30		
Gly	Leu	Gly	Gly	Ala	Pro	Leu	Gly	Leu	Arg	Leu	Pro	Arg	Glu	Thr	Asp
		35					40					45			
Glu	Glu	Pro	Glu	Glu	Pro	Gly	Arg	Arg	Gly	Ser	Phe	Val	Glu	Met	Val
	50					55					60				
Asp	Asn	Leu	Arg	Gly	Lys	Ser	Gly	Gln	Gly	Tyr	Tyr	Val	Glu	Met	Thr
65					70					75					80
Val	Gly	Ser	Pro	Pro	Gln	Thr	Leu	Asn	Ile	Leu	Val	Asp	Thr	Gly	Ser
				85					90					95	
Ser	Asn	Phe	Ala	Val	Gly	Ala	Ala	Pro	His	Pro	Phe	Leu	His	Arg	Tyr
			100					105					110		
Tyr	Gln	Arg	Gln	Leu	Ser	Ser	Thr	Tyr	Arg	Asp	Leu	Arg	Lys	Gly	Val
		115					120					125			
Tyr	Val	Pro	Tyr	Thr	Gln	Gly	Lys	Trp	Glu	Gly	Glu	Leu	Gly	Thr	Asp
	130					135					140				
Leu	Val	Ser	Ile	Pro	His	Gly	Pro	Asn	Val	Thr	Val	Arg	Ala	Asn	Ile
145					150					155					160
Ala	Ala	Ile	Thr	Glu	Ser	Asp	Lys	Phe	Phe	Ile	Asn	Gly	Ser	Asn	Trp
				165					170					175	
Glu	Gly	Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Glu	Ile	Ala	Arg	Pro	Asp	Asp
			180					185					190		
Ser	Leu	Glu	Pro	Phe	Phe	Asp	Ser	Leu	Val	Lys	Gln	Thr	His	Val	Pro
		195					200					205			
Asn	Leu	Phe	Ser	Leu	Gln	Leu	Cys	Gly	Ala	Gly	Phe	Pro	Leu	Asn	Gln
	210					215					220				
Ser	Glu	Val	Leu	Ala	Ser	Val	Gly	Gly	Ser	Met	Ile	Ile	Gly	Gly	Ile
225					230					235					240
Asp	His	Ser	Leu	Tyr	Thr	Gly	Ser	Leu	Trp	Tyr	Thr	Pro	Ile	Arg	Arg
				245					250					255	
Glu	Trp	Tyr	Tyr	Glu	Val	Ile	Ile	Val	Arg	Val	Glu	Ile	Asn	Gly	Gln
			260					265					270		
Asp	Leu	Lys	Met	Asp	Cys	Lys	Glu	Tyr	Asn	Tyr	Asp	Lys	Ser	Ile	Val
		275					280					285			
Asp	Ser	Gly	Thr	Thr	Asn	Leu	Arg	Leu	Pro	Lys	Lys	Val	Phe	Glu	Ala
	290					295					300				
Ala	Val	Lys	Ser	Ile	Lys	Ala	Ala	Ser	Ser	Thr	Glu	Lys	Phe	Pro	Asp
305					310					315					320
Gly	Phe	Trp	Leu	Gly	Glu	Gln	Leu	Val	Cys	Trp	Gln	Ala	Gly	Thr	Thr
			325						330					335	
Pro	Trp	Asn	Ile	Phe	Pro	Val	Ile	Ser	Leu	Tyr	Leu	Met	Gly	Glu	Val
			340					345					350		
Thr	Asn	Gln	Ser	Phe	Arg	Ile	Thr	Ile	Leu	Pro	Gln	Gln	Tyr	Leu	Arg
		355					360					365			
Pro	Val	Glu	Asp	Val	Ala	Thr	Ser	Gln	Asp	Asp	Cys	Tyr	Lys	Phe	Ala

370		375		380
Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu				
385		390		395
Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala				400
	405		410	415
Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu				
	420		425	430
Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro				
	435		440	445
Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala				
	450		455	460
Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp				
465		470		475
Arg Cys Leu Arg Cys Leu Arg Gln Gln His Asp Asp Phe Ala Asp Asp				480
	485		490	495
Ile Ser Leu Leu Lys				
	500			

<210> 3  
 <211> 24  
 <212> DNA  
 <213> Homo sapiens

<400> 3  
 gagagacgar garccwgagg agcc

24

<210> 4  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Degenerate oligonucleotide primer derived from SEQ  
 ID NO: 2

<400> 4  
 gagagacgar garccwgaag agcc

24

<210> 5  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Degenerate oligonucleotide primer derived from SEQ  
 ID NO: 2

<400> 5  
 gagagacgar garccwgaag aacc

24

<210> 6  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Degenerate oligonucleotide primer derived from SEQ  
 ID NO: 2

<400> 6  
 gagagacgar garccwgagg aacc

24

<210> 7  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Degenerate oligonucleotide primer derived from SEQ  
ID NO: 2

<400> 7  
agagacgarg arccsgagga gcc 23

<210> 8  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Degenerate oligonucleotide primer derived from SEQ  
ID NO: 2

<400> 8  
agagacgarg arccsgaaga gcc 23

<210> 9  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Degenerate oligonucleotide primer derived from SEQ  
ID NO: 2

<400> 9  
agagacgarg arccsgaaga acc 23

<210> 10  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Degenerate oligonucleotide primer derived from SEQ  
ID NO: 2

<400> 10  
agagacgarg arccsgagga acc 23

<210> 11  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Degenerate oligonucleotide primer derived from SEQ  
ID NO: 2

<400> 11  
cgtcacagrt trtcaaccat ctc 23

<210> 12  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Degenerate oligonucleotide primer derived from SEQ  
ID NO: 2

<400> 12  
cgtcacagrt trtctaccat ctc 23

<210> 13  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Degenerate oligonucleotide primer derived from SEQ  
ID NO: 2

<400> 13  
cgtcacagrt trtccaccat ctc 23

<210> 14  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Degenerate oligonucleotide primer derived from SEQ  
ID NO: 2

<400> 14  
cgtcacagrt trtcgaccat ctc 23

<210> 15  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Degenerate oligonucleotide primer derived from SEQ  
ID NO: 2

<400> 15  
cgtcacagrt trtcaaccat ttc 23

<210> 16  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Degenerate oligonucleotide primer derived from SEQ  
ID NO: 2

<400> 16  
cgtcacagrt trtctaccat ttc 23

<210> 17

<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Degenerate oligonucleotide primer derived from SEQ  
ID NO: 2

<400> 17  
cgtcacagrt trtccacat ttc 23

<210> 18  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Degenerate oligonucleotide primer derived from SEQ  
ID NO: 2

<400> 18  
cgtcacagrt trtcgacat ttc 23

<210> 19  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Degenerate oligonucleotide primer derived from SEQ  
ID NO: 2

<400> 19  
gaggggcagc tttgtggaga 20

<210> 20  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Degenerate oligonucleotide primer derived from SEQ  
ID NO: 2

<400> 20  
cagcataggc cagccccagg atgcct 26

<210> 21  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Degenerate oligonucleotide primer derived from SEQ  
ID NO: 2

<400> 21  
gtgatggcag caatgttggc acgc 24

<210> 22  
<211> 17

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Degenerate oligonucleotide primer

<221> misc\_feature  
<222> (1)...(17)  
<223> n = A,T,C or G

<400> 22  
gaygargagc cngagga 17

<210> 23  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Degenerate oligonucleotide primer

<221> misc\_feature  
<222> (1)...(17)  
<223> n = A,T,C or G

<400> 23  
gaygargagc cngaaga 17

<210> 24  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Degenerate oligonucleotide primer

<221> misc\_feature  
<222> (1)...(17)  
<223> n = A,T,C or G

<400> 24  
gaygargaac cngagga 17

<210> 25  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Degenerate oligonucleotide primer

<221> misc\_feature  
<222> (1)...(17)  
<223> n = A,T,C or G

<400> 25  
gaygargaac cngaaga 17

<210> 26  
<211> 15  
<212> DNA

<213> Artificial Sequence

<220>

<223> Degenerate oligonucleotide primer

<221> misc\_feature

<222> (1)...(15)

<223> n = A,T,C or G

<400> 26

rttrtcnacc atttc

15

<210> 27

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> Degenerate oligonucleotide primer

<221> misc\_feature

<222> (1)...(15)

<223> n = A,T,C or G

<400> 27

rttrtcnacc atctc

15

<210> 28

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Degenerate oligonucleotide primer

<221> misc\_feature

<222> (1)...(17)

<223> n = A,T,C or G

<400> 28

tcnaccatyt cnacaaa

17

<210> 29

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Degenerate oligonucleotide primer

<221> misc\_feature

<222> (1)...(17)

<223> n = A,T,C or G

<400> 29

tcnaccatyt cnacgaa

17

<210> 30

<211> 27

<212> DNA

<213> Artificial Sequence



<220>  
 <223> Degenerate oligonucleotide primer  
  
 <400> 30  
 atattctaga gaygargagc cagaaga 27  
  
 <210> 31  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Degenerate oligonucleotide primer  
  
 <400> 31  
 atattctaga gaygargagc cggaaga 27  
  
 <210> 32  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Degenerate oligonucleotide primer  
  
 <400> 32  
 atattctaga gaygargagc ccgaaga 27  
  
 <210> 33  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Degenerate oligonucleotide primer  
  
 <400> 33  
 atattctaga gaygargagc ctgaaga 27  
  
 <210> 34  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Degenerate oligonucleotide primer  
  
 <221> misc\_feature  
 <222> (1)...(30)  
 <223> n = A,T,C or G  
  
 <400> 34  
 acacgaattc ttrtcnacca tytcaacaaa 30  
  
 <210> 35  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>

<223> Degenerate oligonucleotide primer

<221> misc\_feature

<222> (1)...(30)

<223> n = A,T,C or G

<400> 35

acacgaattc ttrtcnacca tytcgacaaa

30

<210> 36

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Degenerate oligonucleotide primer

<221> misc\_feature

<222> (1)...(30)

<223> n = A,T,C or G

<400> 36

acacgaattc ttrtcnacca tytccacaaa

30

<210> 37

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Degenerate oligonucleotide primer

<221> misc\_feature

<222> (1)...(30)

<223> n = A,T,C or G

<400> 37

acacgaattc ttrtcnacca tytctacaaa

30

<210> 38

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Degenerate oligonucleotide primer

<400> 38

aagagcccgg ccggaggggc a

21

<210> 39

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Degenerate oligonucleotide primer

<400> 39

aaagctgccc ctccggccgg g

21

<210> 40  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Degenerate oligonucleotide primer

<400> 40  
agctcgttta gtgaaccgtc agatcg

26

<210> 41  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Degenerate oligonucleotide primer

<400> 41  
acctacaggt ggggtctttc attccc

26

<210> 42  
<211> 2348  
<212> DNA  
<213> Homo sapiens

<400> 42  
ccatgccggc ccctcacagc cccgccggga gcccagagccc gctgcccagg ctggccgccc 60  
csgtgccgat gtagcgggct ccggatccca gcctctcccc tgcctccgtg ctctgaggat 120  
ctccccctgac cgctctccac agccccgacc cgggggctgg cccagggccc tgcaggccct 180  
ggcgtcctga tgcccccaag ctccctctcc tgagaagcca ccagcaccac ccagacttgg 240  
gggcaggcgc cagggacgga cgtgggccaag tgcgagccca gagggcccga aggcgggggc 300  
ccaccatggc ccaagccctg ccctggctcc tgctgtggat gggcgcggga gtgctgcctg 360  
cccacggcac ccagcacggc atccggctgc ccctgcgcag cggcctgggg ggcgcccccc 420  
tggggctgcg gctgccccgg gagaccgacg aagagcccga ggagcccggc cggaggggca 480  
gctttgtgga gatggtggac aacctgaggg gcaagtccgg gcagggtac tacgtggaga 540  
tgaccgtggg cagccccccg cagacgctca acatcctggt ggatacaggc agcagtaact 600  
ttgcagtggg tgctgcccc cacccttcc tgcatcgcta ctaccagagg cagctgtcca 660  
gcacataccg ggacctccgg aagggtgtgt atgtgcccta caccagggc aagtgggaag 720  
gggagctggg caccgacctg gtaagcatcc cccatggccc caacgtcact gtgcgtgcca 780  
acattgctgc catcactgaa tcagacaagt tcttcatcaa cggctccaac tgggaaggca 840  
tcctggggct ggcctatgct gagattgcca ggctgacga ctccctggag cttttctttg 900  
actctctggt aaagcagacc caggttccca acctcttctc cctgcagctt tgtggtgctg 960  
gcttccccct caaccagtct gaagtgtggt cctctgtcgg agggagcatg atcattggag 1020  
gtatcgacca ctgctgtac acaggcagtc tctgtatata acccatccgg cgggagtgg 1080  
attatgaggt gatcattgtg cgggtggaga tcaatggaca ggatctgaaa atggactgca 1140  
aggagtacaa ctatgacaag agcattgtgg acagtggcac caccaacctt cgtttgcccc 1200  
agaaagtgtt tgaagctgca gtcaaatacca tcaaggcagc ctctccacg gagaagttcc 1260  
ctgatggttt ctggctagga gagcagctgg tgtgctggca agcaggcacc accccttgg 1320  
acattttccc agtcatctca ctctacctaa tgggtgaggt taccaaccag tccttccgca 1380  
tcaccatcct tccgcagcaa tacctgcggc cagtgggaaga tgtggccacg tcccaagacg 1440  
actgttacaa gtttgccatc tcacagtcac ccacgggcac tgttatggga gctgttatca 1500  
tggagggctt ctacgttgtc tttgatcggg cccgaaaacg aattggcttt gctgtcagcg 1560  
cttgccatgt gcacgatgag ttcaggacgg cagcggtgga aggccctttt gtcaccttgg 1620  
acatggaaga ctgtggctac aacattccac agacagatga gtcaaccctc atgaccatag 1680  
cctatgtcat ggctgccatc tgcgccctct tcatgctgcc actctgcctc atggtgtgtc 1740  
agtggcgtg cctccgctgc ctgcgccagc agcatgatga ctttgctgat gacatctccc 1800  
tgctgaagtg aggaggccca tgggcagaag atagagattc ccctggacca cacctccgtg 1860  
gttcactttg gtcacaagta ggagacacag atggcacctg tggccagagc acctcaggac 1920  
cctccccacc caccaaatac ctctgccttg atggagaagg aaaaggctgg caagggtggg 1980

tccagggact	gtacctgtag	gaaacagaaa	agagaagaaa	gaagcactct	gctggcgggg	2040
atactcttgg	tcacctcaaa	tttaagtcgg	gaaattctgc	tgcttgaaac	ttcagccctg	2100
aacctttgtc	caccattcct	ttaaattctc	caacccaaag	tattcttctt	ttcttagttt	2160
cagaagtact	ggcatcacac	gcaggttacc	ttggcgtgtg	tccctgtggg	accctggcag	2220
agaagagacc	aagcttggtt	ccctgctggc	caaagtcagt	aggagaggat	gcacagtttg	2280
ctatttgctt	tagagacagg	gactgtataa	acaagcctaa	cattggtgca	aagattgcct	2340
cttgaatt						2348

<210> 43  
 <211> 456  
 <212> PRT  
 <213> Homo sapiens

<400> 43

Glu	Thr	Asp	Glu	Glu	Pro	Glu	Glu	Pro	Gly	Arg	Arg	Gly	Ser	Phe	Val
1			5						10					15	
Glu	Met	Val	Asp	Asn	Leu	Arg	Gly	Lys	Ser	Gly	Gln	Gly	Tyr	Tyr	Val
			20					25					30		
Glu	Met	Thr	Val	Gly	Ser	Pro	Pro	Gln	Thr	Leu	Asn	Ile	Leu	Val	Asp
			35				40					45			
Thr	Gly	Ser	Ser	Asn	Phe	Ala	Val	Gly	Ala	Ala	Pro	His	Pro	Phe	Leu
			50			55					60				
His	Arg	Tyr	Tyr	Gln	Arg	Gln	Leu	Ser	Ser	Thr	Tyr	Arg	Asp	Leu	Arg
					70					75					80
Lys	Gly	Val	Tyr	Val	Pro	Tyr	Thr	Gln	Gly	Lys	Trp	Glu	Gly	Glu	Leu
				85					90					95	
Gly	Thr	Asp	Leu	Val	Ser	Ile	Pro	His	Gly	Pro	Asn	Val	Thr	Val	Arg
			100					105					110		
Ala	Asn	Ile	Ala	Ala	Ile	Thr	Glu	Ser	Asp	Lys	Phe	Phe	Ile	Asn	Gly
			115				120					125			
Ser	Asn	Trp	Glu	Gly	Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Glu	Ile	Ala	Arg
			130			135					140				
Pro	Asp	Asp	Ser	Leu	Glu	Pro	Phe	Phe	Asp	Ser	Leu	Val	Lys	Gln	Thr
					150					155					160
His	Val	Pro	Asn	Leu	Phe	Ser	Leu	Gln	Leu	Cys	Gly	Ala	Gly	Phe	Pro
				165					170					175	
Leu	Asn	Gln	Ser	Glu	Val	Leu	Ala	Ser	Val	Gly	Gly	Ser	Met	Ile	Ile
			180					185					190		
Gly	Gly	Ile	Asp	His	Ser	Leu	Tyr	Thr	Gly	Ser	Leu	Trp	Tyr	Thr	Pro
			195				200					205			
Ile	Arg	Arg	Glu	Trp	Tyr	Tyr	Glu	Val	Ile	Ile	Val	Arg	Val	Glu	Ile
			210			215					220				
Asn	Gly	Gln	Asp	Leu	Lys	Met	Asp	Cys	Lys	Glu	Tyr	Asn	Tyr	Asp	Lys
					230					235					240
Ser	Ile	Val	Asp	Ser	Gly	Thr	Thr	Asn	Leu	Arg	Leu	Pro	Lys	Lys	Val
				245					250					255	
Phe	Glu	Ala	Ala	Val	Lys	Ser	Ile	Lys	Ala	Ala	Ser	Ser	Thr	Glu	Lys
			260					265					270		
Phe	Pro	Asp	Gly	Phe	Trp	Leu	Gly	Glu	Gln	Leu	Val	Cys	Trp	Gln	Ala
			275				280					285			
Gly	Thr	Thr	Pro	Trp	Asn	Ile	Phe	Pro	Val	Ile	Ser	Leu	Tyr	Leu	Met
			290			295					300				
Gly	Glu	Val	Thr	Asn	Gln	Ser	Phe	Arg	Ile	Thr	Ile	Leu	Pro	Gln	Gln
				310					315						320
Tyr	Leu	Arg	Pro	Val	Glu	Asp	Val	Ala	Thr	Ser	Gln	Asp	Asp	Cys	Tyr
				325					330					335	
Lys	Phe	Ala	Ile	Ser	Gln	Ser	Ser	Thr	Gly	Thr	Val	Met	Gly	Ala	Val
			340					345					350		
Ile	Met	Glu	Gly	Phe	Tyr	Val	Val	Phe	Asp	Arg	Ala	Arg	Lys	Arg	Ile
			355				360					365			
Gly	Phe	Ala	Val	Ser	Ala	Cys	His	Val	His	Asp	Glu	Phe	Arg	Thr	Ala

370	Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met	375	Glu Asp Cys Gly Tyr
385	Asn Ile Pro Gln Thr Asp Glu Ser Thr Leu Met	390	Thr Ile Ala Tyr Val
		405	415
	Met Ala Ala Ile Cys Ala Leu Phe Met Leu Pro	410	Leu Cys Leu Met Val
		420	430
	Cys Gln Trp Arg Cys Leu Arg Cys Leu Arg Gln	425	Gln His Asp Asp Phe
		440	445
	Ala Asp Asp Ile Ser Leu Leu Lys		
	450	455	

<210> 44  
 <211> 2348  
 <212> DNA  
 <213> Homo sapiens

<400> 44

ccatgccggc	ccctcacagc	cccgcgggga	gcccagagccc	gctgcccagg	ctggccgccc	60
csgtgccgat	gtagcgggct	ccggatccca	gcctctcccc	tgctcccgtg	ctctgcggat	120
ctcccctgac	cgctctccac	agccccggacc	ggggggctgg	cccaggggccc	tgccagccct	180
ggcgtcctga	tgcccccaag	ctccctctcc	tgagaagcca	ccagcaccac	ccagacttgg	240
gggcaggcgc	cagggacgga	cgtgggccag	tgcgagccca	gagggcccga	aggccggggc	300
ccaccatggc	ccaagccctg	ccctggctcc	tgctgtggat	gggcgcggga	gtgctgcctg	360
cccacggcac	ccagcacggc	atccggctgc	ccctgcgcag	cggcctgggg	ggcgcggccc	420
tggggctgcg	gctgccccgg	gagaccgacg	aagagcccga	ggagcccggc	cggaggggca	480
gctttgtgga	gatggtggac	aacctgaggg	gcaagtccgg	gcagggctac	tacgtggaga	540
tgaccgtggg	cagccccccc	cagacgctca	acatcctggt	ggatacaggc	agcagtaact	600
ttgcagtggg	tgctgcccc	cacccttcc	tgcatcgcta	ctaccagagg	cagctgtcca	660
gcacataccg	ggacctccgg	aagggtgtgt	atgtgcccta	caccagggc	aagtgggaag	720
gggagctggg	caccgacctg	gtaagcatcc	cccatggccc	caacgtcaact	gtgcgtgcca	780
acattgctgc	catcactgaa	tcagacaagt	tcttcatcaa	cggctccaac	tgggaaggca	840
tcctggggct	ggcctatgct	gagattgcca	ggcctgacga	ctccctggag	cctttctttg	900
actctctggt	aaagcagacc	cacgttccca	acctcttctc	cctgcagctt	tgtggtgctg	960
gcttccccct	caaccagtct	gaagtgtctg	cctctgtcgg	agggagcatg	atcattggag	1020
gtatcgacca	ctcgtgttac	acaggcagtc	tctggtatac	acccatccgg	cgggagtggg	1080
attatgaggt	gatcattgtg	cgggtggaga	tcaatggaca	ggatctgaaa	atggactgca	1140
aggagtacaa	ctatgacaag	agcattgttg	acagtggcac	caccaacctt	cgtttgccc	1200
agaaagtgtt	tgaagctgca	gtcaaatcca	tcaaggcagc	ctcctccacg	gagaagtcc	1260
ctgatggttt	ctggctagga	gagcagctgg	tgtgctggca	agcaggcacc	accccttgga	1320
acattttccc	agtcattctc	ctctacctaa	tgggtgaggt	taccaaccag	tccttccgca	1380
tcaccatcct	tccgcagcaa	tacctgcggc	cagtgggaag	tgtggccacg	tcccaagacg	1440
actgttacaa	gtttgccatc	tcacagtcac	ccacgggcac	tggttatggg	gctgttatca	1500
tggagggtct	ctacgtttgc	tttgatcggg	cccgaacacg	aattggcttt	gctgtcagcg	1560
cttgccatgt	gcacgatgag	ttcaggacgg	cagcgggtga	aggccctttt	gtcaccttgg	1620
acatggaaga	ctgtggctac	aacattccac	agacagatga	gtcaaccctc	atgaccatag	1680
cctatgtcat	ggctgccatc	tgcgccctct	tcattgtgcc	actctgcctc	atggtgtgtg	1740
agtggcgctg	cctccgctgc	ctgcgccagc	agcatgatga	ctttgctgat	gacatctccc	1800
tgctgaagtg	aggaggccca	tgggcagaag	atagagattc	ccctggacca	cacctccgtg	1860
gttcactttg	gtcacaagta	ggagacacag	atggcacctg	tggccagagc	acctcaggac	1920
cctccccacc	caccaaattg	ctctgccttg	atggagaagg	aaaaggctgg	caagggtggg	1980
tccagggtact	gtacctgtag	gaaacagaaa	agagaagaaa	gaagcactct	gctggcgagg	2040
atactcttgg	tcacctcaaa	tttaagtcgg	gaaattctgc	tgcttgaaac	ttcagccctg	2100
aacctttgtc	caccattcct	ttaaattctc	caacccaaag	tattcttctt	ttcttagttt	2160
cagaagtact	ggcatcacac	gcagggttacc	ttggcgtgtg	tcctgtgggt	acctcggcag	2220
agaagagacc	aagcttggtt	ccctgctggc	caaagtcagt	aggagaggat	gcacagtttg	2280
ctatttgctt	tagagacagg	gactgtataa	acaagcctaa	cattggtgca	aagattgcct	2340
cttgaatt						2348

<210> 45  
 <211> 7

<212> PRT  
<213> Artificial Sequence

<220>  
<223> Flag sequence

<400> 45  
Tyr Lys Asp Asp Asp Asp Lys  
1 5

<210> 46  
<211> 22  
<212> PRT  
<213> Homo sapiens

<400> 46  
Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val  
1 5 10 15  
Leu Pro Ala His Gly Thr  
20

<210> 47  
<211> 23  
<212> PRT  
<213> Homo sapiens

<400> 47  
Gln His Gly Ile Arg Leu Pro Leu Arg Ser Gly Leu Gly Gly Ala Pro  
1 5 10 15  
Leu Gly Leu Arg Leu Pro Arg  
20

<210> 48  
<211> 16080  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Expression Vector pCEK

<221> misc\_feature  
<222> (1)...(16080)  
<223> n = A,T,C or G

<400> 48  
ttctcatggt tgacagctta tcatcgaga tccgggcaac gttgttgcat tgctgcaggc 60  
gcagaactgg taggtatgga agatccgatg tacggggccag atatacgcg tgacattgat 120  
tattgactag ttattaatag taatcaatta cgggggtcatt agttcatagc ccatatatgg 180  
agttccgcgt tacataactt acggtaaagt gcccgcctgg ctgaccgccc aacgaccccc 240  
gccattgac gtcaataatg acgtatgttc ccatagtaac gccaataggg actttccatt 300  
gacgtcaatg ggtggactat ttacggtaaa ctgcccactt ggaggtacat caagtgtatc 360  
atatgccaa g tacgccccct attgacgtca atgacggtaa atggcccggc tggcattatg 420  
cccagttacat gaccttatgg gactttccta cttggcagta catctacgta ttagtcatcg 480  
ctattaccat ggtgatgcgg ttttggcagt acatcaatgg gcgtggatag cggtttgact 540  
cacgggggatt tccaagtctc caccacattg acgtcaatgg gagtttggtt tggcaccaaa 600  
atcaacggga ctttccaaaa tgctgtaaca actccgcccc attgacgcaa atgggcggta 660  
ggcgtgtacg gtgggaggtc tatataagca gagctctctg gctaactaga gaaccactg 720  
cttactggct tatcgaaatt aatacgactc actataggga gaccaagct ctgttgggct 780  
cgcggttgag gacaaactct tcgcggtctt tccagtactc ttggatcgga aaccgcgcgg 840  
cctccgaacg gtactccggc accgagggac ctgagcgagt ccgcatcgac cggatcggaa 900  
aacctctcga ctgttggggg gagtactccc tctcaaaagc gggcatgact tctgcgctaa 960

gattgtcagt	ttccaaaaac	gaggaggatt	tgatattcac	ctggcccgcg	gtgatgcctt	1020
tgaggggtggc	cgcgtccatc	tggtcagaaa	agacaatctt	tttgttgtca	agcttgagggt	1080
gtggcagggt	tgagatctgg	ccatacactt	gagtgacaat	gacatccact	ttgcctttct	1140
ctccacaggt	gtccactccc	aggtccaact	gcaggtcgac	tctagaccgc	gggaattctg	1200
cagatatcca	tcacactggc	cgcactcgtc	cccagcccgc	ccgggagctg	cgagccgcga	1260
gctggattat	ggtggcctga	gcagccaacg	cagccgcagg	agcccggagc	ccttgcccct	1320
gcccgcgcgc	ccgcccgcgc	gggggaccag	ggaagccgcc	accggcccgc	catgcccgcg	1380
cctcccagcc	ccgcccggag	cccgcgcccg	ctgcccaggc	tgccgcgcgc	cgtgccgatg	1440
tagcgggctc	cggatcccag	cctctcccct	gctcccgtgc	tctgcggatc	tcccctgacc	1500
gctctccaca	gcccggaccc	gggggctggc	ccagggccct	gcaggccctg	gcgtcctgat	1560
gcccccaagc	tcccctctct	gagaagccac	cagcaccacc	cagacttggg	ggcaggcgcc	1620
agggacggac	gtgggccaagt	gcgagcccag	agggcccga	ggccggggcc	caccatggcc	1680
caagccctgc	cctggctcct	gctgtggatg	ggcgcgggag	tgctgcctgc	ccacggcacc	1740
cagcacggca	tccggctgcc	cctgcgcagc	ggcctggggg	gcgccccct	ggggctgcgg	1800
ctgccccggg	agaccgacga	agagcccag	gagcccggcc	ggaggggcag	ctttgtggag	1860
atggtggaca	acctgagggg	caagtcgggg	cagggtact	acgtggagat	gaccgtgggc	1920
agccccccgc	agacgtcaa	catcctggtg	gatacaggca	gcagtaactt	tgagtgagg	1980
gctgcccccc	accccttctt	gcacgcctac	taccagaggc	agctgtccag	cacataccgc	2040
gacctccgga	aggtgtgta	tgtgccctac	acccagggca	agtgggaagg	ggagctgggc	2100
accgacctgg	taagcatccc	ccatggcccc	aacgtcactg	tgctgcca	cattgctgcc	2160
atcactgaat	cagacaagtt	cttcatcaac	ggctccaact	gggaaggcat	cctggggctg	2220
gcctatgctg	agattgccag	gcctgacgac	tccctggagc	ctttctttga	ctctctggta	2280
aagcagaccc	acgttcccaa	cctcttctcc	ctgcagcttt	tggtgtctgg	cttccccctc	2340
aaccagtctg	aagtgtctgg	ctctgtcgga	gggagcatga	tcattggagg	tatcgaccac	2400
tcgctgtaca	caggcagctt	ctggtataca	cccatccggc	gggagtggtg	ttatgaggtc	2460
atcattgtgc	gggtggagat	caatggacag	gatctgaaaa	tgactgcaa	ggagtacaac	2520
tatgacaaga	gcattgtgga	cagtggcacc	accaaccttc	gtttgcccga	gaaagtgttt	2580
gaagctgcag	tcaaatccat	caaggcagcc	tcttccacgg	agaagttccc	tgatggtttc	2640
tggtctaggag	agcagctggt	gtgctggcaa	gcaggcacca	ccccttgga	cattttccca	2700
gtcatctcac	tctaccta	gggtgaggtt	accaaccagt	ccttccgc	caccatcctt	2760
ccgcagcaat	acctgcggcc	agtggaagat	gtggccacgt	cccaagacga	ctgttacaag	2820
tttgccatct	cacagtcac	cacgggcact	gttatgggag	ctgttatcat	ggagggcttc	2880
tacgttgtct	ttgatcgggc	ccgaaaacga	attggctttg	ctgtcagcgc	ttgccatgtg	2940
cacgatgagt	tcaggacggc	agcgggtggaa	ggcccttttg	tcaccttga	catggaagac	3000
tgtggctaca	acattccaca	gacagatgag	tcaacctca	tgaccatagc	ctatgtcatg	3060
gctgccatct	gcgcctctt	catgctgcca	ctctgcctca	tggtgtgtca	gtggcgctgc	3120
ctccgctgcc	tgccgacga	gcctgatgac	tttgcctgatg	acatctccct	gctgaagtga	3180
ggaggcccat	gggcagaaga	tagagattcc	cctggaccac	acctccgtgg	ttacttttgg	3240
tcacaagtag	gagacacaga	tgccacctgt	ggccagagca	cctcaggacc	ctccccaccc	3300
accaaagtcc	tctgccttga	tgagagaagg	aaaggctggc	aaggtgggtt	ccagggactg	3360
tacctgtagg	aaacagaaaa	gagaagaaag	aagcactctg	ctggcgggaa	tactcttggg	3420
cacctcaa	ttaaagtcggg	aaattctgct	gcttgaaact	tcagccctga	acctttgtcc	3480
accattcctt	taaattctcc	aaoccaaagt	attcttcttt	tcttagtttc	agaagtactg	3540
gcacacacg	caggttacct	tggcgtgtgt	ccctgtggta	ccctggcaga	gaagagacca	3600
agcttgtttc	cctgctggcc	aaagtcagta	ggagaggatg	cacagtttgc	tatttgcctt	3660
agagacaggg	actgtataaa	caagccta	attggtgcaa	agattgcctc	ttgaattaaa	3720
aaaaaaaaact	agattgacta	tttatacaaa	tgggggcggc	tgaaagagg	agaaggagag	3780
ggagtacaaa	gacagggaat	agtgggatca	aagctaggaa	aggcagaaac	acaaccactc	3840
accagtccta	gttttagacc	tcatctccaa	gatagcatcc	catctcagaa	gatgggtgtt	3900
gttttcaatg	ttttcttttc	tgtggttgca	gcctgacc	aagtgagatg	ggaagggtct	3960
atctagccaa	agagctcttt	tttagctctc	ttaaatgaag	tgccactaa	gaagttccac	4020
ttaacacatg	aatttctgcc	atattaattt	cattgtctct	atctgaacca	ccctttattc	4080
tacatatgat	aggcagcact	gaaatatcct	aacccctaa	gctccagggtg	ccctgtggga	4140
gagcaactgg	actatagcag	ggctgggctc	tgtcttctct	gtcataggct	cactctttcc	4200
cccaaactct	cctctggagc	tttgacgcca	aggtgctaaa	aggaatagg	aggagacctc	4260
ttctatctaa	tccttaaaag	cataatgttg	aacattcatt	caacagctga	tgccctataa	4320
cccctgcctg	gatttcttcc	tattaggcta	taagaagtag	caagatcttt	acataattca	4380
gagtggtttc	attgccttcc	tacctctct	aatggccct	ccatttattt	gactaaagca	4440
tcacacagtg	gcactagcat	tataccaaga	gtatgagaaa	tacagtgtct	tatggctcta	4500
acattactgc	cttcagtatc	aaggctgcct	ggagaaagga	tggcagcctc	agggttctct	4560
tatgtcctcc	accacaagag	ctccttgatg	aaggtcatct	ttttccctca	tcctgttctt	4620

ccccccccg	ctcctaattg	tacgtgggta	cccaggctgg	ttcttgggct	aggtagtg	4680
gaccaagtcc	attacctccc	tatcagttct	agcatagtaa	actacggtag	cagtgttagt	4740
gggaagagct	gggttttcc	agtataccca	ctgcaccta	ctcctacctg	gtcaaccgcg	4800
tgcttccagg	tatgggacct	gctaagtggt	gaattacctg	ataagggaga	gggaaataca	4860
aggagggcct	ctgggtgttc	tggcctcagc	cagctgcccc	caagccataa	accaataaaa	4920
caagaatact	gagtcagttt	tttatctggg	ttctcttcat	tcccactgca	cttgggtgctg	4980
ctttggctga	ctgggaacac	cccataacta	cagagtctga	caggaagact	ggagactgtc	5040
cacttctagc	tcggaactta	ctgtgtaaat	aaactttcag	aactgctacc	atgaagtga	5100
aatgccacat	tttgctttat	aatttctacc	catgttggga	aaaactggct	ttttcccagc	5160
cctttccagg	gcataaaaact	caaccccttc	gacagcaagt	cccatcagcc	tattattttt	5220
ttaaagaaaa	cttgcaacttg	tttttctttt	tacagttact	tccttctctg	cccaaaatta	5280
taaactctaa	gtgtaaaaaa	aagtcttaac	aacagcttct	tgcttgtaaa	aatatgtatt	5340
atacatctgt	attttttaaat	tctgtctctg	aaaaatgact	gtcccattct	ccactcactg	5400
catttggggc	ctttcccatt	ggtctgcatg	tcttttatca	ttgcaggcca	gtggacagag	5460
ggagaaggga	gaacaggggt	cgccaacact	tgtgttgctt	tctgactgat	cctgaacaag	5520
aaagagttaac	actgaggcgc	tcgtctccat	gcacaactct	ccaaaacact	tatctctctg	5580
caagagtggg	ctttccgggt	ctttactggg	aagcagttaa	gccccctcct	caccccttcc	5640
ttttttcttt	ctttactcct	ttggcttcaa	aggatttttg	aaaagaaaca	atatgcttta	5700
cactcatttt	caatttctaa	atttgcaggg	gatactgaaa	aatacggcag	gtggcctaag	5760
gctgctgtaa	agttgagggg	agaggaaatc	ttaagattac	aagataaaaa	acgaatcccc	5820
taaacaaaaa	gaacaataga	actggtcttc	cattttgcc	cctttctctg	tcatgacagc	5880
tactaacctg	gagacagtaa	catttccatta	accaaagaaa	gtgggtcacc	tgacctctga	5940
agagctgagt	actcaggcca	ctccaatcac	cctacaagat	gccaaggagg	tcccagggaag	6000
tccagctcct	taaactgacg	ctagtcaata	aacctgggca	agtgaggcaa	gagaaatgag	6060
gaagaatcca	tctgtgaggt	gacaggcacg	gatgaaagac	aaagacggaa	aagagtatca	6120
aaggcagaaa	ggagatcatt	tagttgggtc	tgaaaggaaa	agtntttgct	atccgacatg	6180
tactgctagt	wcctgtaagc	attttaggtc	ccagaatgga	aaaaaaaaatc	aagctatngg	6240
ttatataata	atgnnnnnnn	nnnnnnnnnn	nntcgagcat	gcacttagag	ggccctattc	6300
tatagtgtca	cctaattgct	agagctcgct	gacagcctc	gactgtgcct	tctagttgcc	6360
agccatctgt	tgtttgcccc	tcccccgctg	cttccttgac	cctggaaggt	gccactccca	6420
ctgtcctttc	ctaataaaat	gaggaaattg	catcgcatgt	tctgagtagg	tgctattcta	6480
ttctgggggg	tgggggtggg	caggacagca	agggggagga	ttgggaagac	aatagcaggc	6540
atgctgggga	tgcgggtggc	tctatggctt	ctgaggcgga	aagaaccagc	tggggctcta	6600
gggggtatcc	ccacgcgccc	tgtagcgggc	cattaagcgc	ggcgggtgtg	gtgggttacgc	6660
gcagcgtgac	cgctacactt	gccagcgccc	tagcgcccgc	tcctttcgct	ttcttccctt	6720
cctttctcgc	cagtttcgcc	ggctttcccc	gtcaagctct	aaatcggggc	atccctttag	6780
ggttccgatt	tagtgcttta	cggcacctcg	accccaaaaa	acttgattag	ggtgatgggt	6840
cacgtagtgg	gccatcgccc	tgatagacgg	tttttcgccc	tttgacgttg	gagtcocagt	6900
tctttaatag	tggactcttg	ttccaaactg	gaacaacact	caaccctatc	tcgggtctatt	6960
cttttgattt	ataagggatt	ttggggattt	cggcctattg	gttaaaaaat	gagctgattt	7020
aacaaaaaatt	taacgcgaat	tctagagccc	cggcgccgga	cgaactaaac	ctgactacgg	7080
catctctgcc	ccttcttcgc	ggggcagtg	atgtaatccc	ttcagttggt	tgggtacaact	7140
tgccaaactgg	gccctgttcc	acatgtgaca	cgggggggga	ccaaacacaa	aggggttctc	7200
tgactgtagt	tgacatcctt	ataaatggat	gtgcacattt	gccaacactg	agtggctttc	7260
atcctggagc	agactttgca	gtctgtggac	tgcaacacaa	cattgccttt	atgtgtaact	7320
cttggtgtaa	gctcttacac	caatgctggg	ggcaggttac	ctcccagggg	cccaggaaga	7380
ctacgggagg	ctacaccaac	gtcaatcaga	ggggcctgtg	tagctaccga	taagcggacc	7440
ctcaagaggg	cattagcaat	agtgtttata	aggccccctt	gttaacccta	aacgggtagc	7500
atatgcttcc	cgggtagtag	tatatactat	ccagactaac	cctaattcaa	tagcatatgt	7560
taccaaacgg	gaagcatatg	ctatcgaaat	agggtagtag	aaagggtcct	aaggaacagc	7620
gatatctccc	accccatgag	ctgtcacggg	tttatttaca	tggggtcagg	attccacgag	7680
ggtagtgaa	catttttagtc	acaagggcag	tggctgaaga	tcaaggagcg	ggcagtgaa	7740
tctcctgaat	cttcgcctgc	ttcttcatte	tccttcgttt	agctaataga	ataactgctg	7800
agttgtgaac	agtaagggtg	atgtgaggtg	ctcgaaaaca	aggtttcagg	tgacgcccc	7860
agaataaaa	ttggacgggg	ggttcagtg	tggcattgtg	ctatgacacc	aatataacc	7920
tcacaataccc	cttgggcaat	aaatactagt	gtaggaatga	aacattctga	atatctttta	7980
caatagaaat	ccatgggggtg	gggacaagcc	gtaaagactg	gatgtccatc	tcacacgaat	8040
ttatggctat	gggcaacaca	taatcctagt	gcaatatgat	actgggggtta	ttaagatgtg	8100
tcccaggcag	ggaccaagac	aggtgaacca	tgttgttaca	ctctattttgt	aacaagggga	8160
aagagagtgg	acgcccagac	cagcggactc	cactggttgt	ctctaaccac	ccgaaaaatt	8220
aaacggggct	ccacgccaat	ggggcccata	aacaaagaca	agtggccact	cttttttttg	8280



aaattgtgga	gtggggggcac	gcgtcagccc	ccacacgccg	ccctgcgggt	ttggactgta	8340
aaataaggg	gtaataactt	ggctgattgt	aaccccgcta	accactgcgg	tcaaaccact	8400
tgcccacaaa	accactaatg	gcaccccggg	gaatacctgc	ataagtaggt	gggcgggcca	8460
agataggggc	gcgattgctg	cgatctggag	gacaaattac	acacacttgc	gcctgagcgc	8520
caagcacagg	gttgttggtc	ctcatattca	cgaggctcgt	gagagcacgg	tgggctaattg	8580
ttgccatggg	tagcatatac	tacccaaata	tctggatagc	atatgctatc	ctaattctata	8640
tctgggtagc	ataggctatc	ctaattctata	tctgggtagc	atatgctatc	ctaattctata	8700
tctgggtagt	atatgctatc	ctaatttata	tctgggtagc	ataggctatc	ctaattctata	8760
tctgggtagc	atatgctatc	ctaattctata	tctgggtagt	atatgctatc	ctaattctgta	8820
tccgggtagc	atatactacc	caaatactctg	ttagggtagt	atatgctatc	ctaatttata	8880
tctgggtagc	atatactacc	caaatactctg	gtagcatat	gctatcctaa	tctatatctg	8940
ggtagcatat	gctatcctaa	tctatatctg	ggtagcatag	gctatcctaa	tctatatctg	9000
ggtagcatat	gctatcctaa	tctatatctg	ggtagtatat	gctatcctaa	tttatatctg	9060
ggtagcatag	gctatcctaa	tctatatctg	ggtagcatat	gctatcctaa	tctatatctg	9120
ggtagtatat	gctatcctaa	tctgtatccg	ggtagcatat	gctatcctca	tgcataataca	9180
gtcagcatat	gatacccgat	agtagagtgg	gagtgcctatc	ctttgcataat	gccgccacct	9240
ccaaggggg	cgtgaatttt	cgctgcttgt	ccttttctctg	catgctgggt	gctcccatte	9300
ttaggtgaat	ttaaggaggc	caggctaaag	ccgtcgcatg	tctgattgct	caccaggtaa	9360
atgtcgctaa	tgttttccaa	cgcgagaagg	tggtgagcgc	ggagctgagt	gacgtgacaa	9420
catgggtatg	cccaattgcc	ccatggtggg	aggacgaaaa	tggtgacaag	acagatggcc	9480
agaaatacac	caacagcacg	catgatgtct	actggggatt	tattcttttag	tgcgggggaa	9540
tacacgggctt	ttaatacgat	tgagggcgtc	tcctaacaag	ttacatcaact	cctgcccttc	9600
ctcaccctca	tctccatcac	ctccttcac	tccgtcatct	ccgtcatcac	cctccgcggc	9660
agccccttcc	accataggtg	gaaaccaggg	aggcaaactc	actccatcgt	caaagctgca	9720
cacagtcacc	ctgatattgc	aggtaggagc	gggctttgtc	ataacaaggt	ccttaatcgc	9780
atccttcaaa	acctcagcaa	atatatgagt	ttgtaaaaag	accatgaaat	aacagacaat	9840
ggactccctt	agcggggccag	gttgtggggc	gggtccaggg	gccattccaa	aggggagacg	9900
actcaatgg	gtaagacgac	attgtggaat	agcaagggca	gttccctcgc	ttaggttgta	9960
aagggagggt	ttactacctc	catatacgaa	cacaccggcg	acccaagttc	cctcgtgggt	10020
agtcctttct	acgtgactcc	tagccaggag	agctcttaaa	ccttctgcaa	tgttctcaaa	10080
tttcgggttg	gaacctcctt	gaccacgatg	ctttccaaac	cacctcctt	ttttgcgcct	10140
gcctccatca	ccctgacccc	gggtccaggt	gcttgggcct	tctcctgggt	catctgcggg	10200
gccctgctct	atcgctcccg	ggggcacgtc	aggctcacca	tctgggccac	cttcttggtg	10260
gtattcaaaa	taatcggtt	cccctacagg	gtggaaaaat	ggccttctac	ctggaggggg	10320
cctgcgcgg	ggagaccggg	atgatgatga	ctgactactg	ggactcctgg	gcctcttttc	10380
tccacgtcca	cgacctctcc	ccctggctct	ttcacgaact	ccccccctgg	ctctttcacg	10440
tccctacccc	cgggggcctc	cactaacctc	tcgaccccg	cctccactac	ctcctcgacc	10500
ccggcctcca	ctgcctcctc	gacccgggcc	tccacctcct	gctcctgccc	ctcctgctcc	10560
tgcctcctct	cctgctcctg	cccctcctgc	ccctcctgct	cctgcccctc	ctgcccctcc	10620
tgtcctgccc	cctcctgccc	ctcctgctcc	tgcccctcct	gcccctcctc	ctgtcctgc	10680
ccctcctgccc	cctcctcctg	ctcctgcccc	tccctgcccct	cctgtcctg	cccctcctgc	10740
ccctcctgct	cctgcccctc	ctgcccctcc	tgctcctgccc	cctcctgctc	ctgcccctcc	10800
tgtcctgccc	cctcctgctc	ctgcccctcc	tgcccctcct	gcccctcctc	ctgtcctgc	10860
ccctcctgct	cctgcccctc	ctgcccctcc	tgcccctcct	gctcctgccc	ctcctcctgc	10920
tccctgcccct	cctgcccctc	ctgcccctcc	tccctgctcct	gcccctcctg	cccctcctcc	10980
tgtcctgccc	cctcctcctg	ctcctgcccc	tccctgcccct	cctgcccctc	cctcctgctc	11040
tgcccctcct	gcccctcctc	ctgtcctgccc	ccctcctcct	gctcctgccc	ctcctgcccc	11100
tccctgcccct	cctcctgctc	ctgcccctcc	tccctgctcct	gcccctcctg	cccctcctgc	11160
ccctcctgccc	cctcctcctg	ctcctgcccc	tccctcctgct	cctgcccctc	ctgtcctgc	11220
ccctcccctg	cctgtcctg	ctcctgttcc	accgtgggtc	cctttgcagc	caatgcaact	11280
tggacgtttt	tgggggtctcc	ggacaccatc	tctatgtctt	ggccctgatc	ctgagccgcc	11340
cgggggtcct	ggtcttccgc	ctcctcgctcc	tgcctccttt	ccccgtcctc	gtccatgggt	11400
atcacccccc	cttcttttag	gtccactgcc	gccggagcct	tctgggtccag	atgtgtctcc	11460
cttctctcct	aggccatttc	caggctcctgt	acctggcccc	tcgtcagaca	tgattcacac	11520
taaaagagat	caatagacat	ctttattaga	cgacgtctag	tgaatacagg	gagtgacagac	11580
tccgtgcccc	tccaacagcc	ccccaccct	catccctctc	atggctcgctg	tcagacagat	11640
ccaggtctga	aaattcccca	tccctccgaac	catcctcgctc	ctcatcacca	attactcgca	11700
gcccggaaaa	ctcccgtctga	acatcctcaa	gatttgctgc	ctgagcctca	agccaggcct	11760
caaattcctc	gtcccccttt	ttgctggacg	gtagggatgg	ggattctcgg	gacccctcct	11820
cttctccttc	aaggtcacca	gacagagatg	ctactggggc	aacggaagaa	aagctgggtg	11880
cggcctgtga	ggatcagctt	atcgatgata	agctgtcaaa	catgagaatt	cttgaagacg	11940

aaagggcctc	gtgatacgcc	tatTTTTata	ggttaatgtc	atgataataa	tggTTTTctta	12000
gacgtcaggt	ggcactTTTT	ggggaaatgt	gcgcggaacc	cctatttTgt	tatTTTTcta	12060
aatacattca	aatatgtatc	cgctcatgag	acaataaccc	tgataaatgc	ttcaataata	12120
ttgaaaaagg	aagagtatga	gtattcaaca	tttccgtgtc	gcccttattc	cctTTTTtgc	12180
ggcatttttg	cttctgtttt	ttgctcacc	agaaacgctg	gtgaaagtaa	aagatgctga	12240
agatcagttg	ggtgcacgag	tgggttacat	cgaactggat	ctcaacagcg	gtaagatcct	12300
tgagagtttt	cgccccgaag	aacgttttcc	aatgatgagc	acttttaaag	ttctgctatg	12360
tggcgcggt	ttatcccggt	ttgacgccc	gcaagagcaa	ctcggtcgcc	gcatacacta	12420
ttctcagaat	gacttggttg	agtactcacc	agtcacagaa	aagcatctta	cggatggcat	12480
gacagtaaga	gaattatgca	gtgctgccat	aacctagagt	gataacactg	cggccaactt	12540
acttctgaca	acgatcggag	gaccgaagga	gctaaccgct	tttttgaca	acatggggga	12600
tcatgtaaat	cgccttgatc	gttgggaacc	ggagctgaat	gaagccatac	caaacgacga	12660
gcgtgacacc	acgatgcctg	cagcaatggc	aacaacgttg	cgaaaactat	taactggcga	12720
actacttact	ctagcttccc	ggcaacaatt	aatagactgg	atggaggcgg	ataaagttgc	12780
aggaccactt	ctgcgctcgg	cccttccggc	tggctggttt	attgctgata	aatctggagc	12840
cggtgagcgt	gggtctcgg	gtatcattgc	agcactgggg	ccagatggta	agccctccc	12900
tatcgtagtt	atctacacga	cggggagtca	ggcaactatg	gatgaacgaa	atagacagat	12960
cgctgagata	ggtgcctcac	tgattaagca	ttggttaactg	tcagaccaag	tttactcata	13020
tatactttaag	attgatttaa	aacttccattt	ttaatttaaa	aggatctagg	tgaagatcct	13080
ttttgataat	ctcatgacca	aaatccctta	acgtgagttt	tcgttccact	gagcgtcaga	13140
ccccgtagaa	aagatcaaag	gatcttcttg	agatcctttt	tttctgcg	taatctgctg	13200
cttgcaaaaca	aaaaaacac	cgctaccagc	ggtggtttgt	ttgccggatc	aagagctacc	13260
aactcttttt	ccgaaggtaa	ctggcttcag	cagagcgcag	ataccaaata	ctgtccttct	13320
agtgtagccg	tagttaggcc	accacttcaa	gaactctgta	gcaccgccta	catacctcgc	13380
tctgctaata	ctgttaccag	tggctgctgc	cagtggcgat	aagtcgtgtc	ttaccgggtt	13440
ggactcaaga	cgatagttac	cggataaggc	gcagcggtcg	ggctgaacgg	ggggttcgtg	13500
cacacagccc	agcttgagc	gaacgacct	caccgaactg	agatacctac	agcgtgagct	13560
atgagaaagc	gccacgcttc	ccgaaggagg	aaaggcggac	aggtatccgg	taagcggcag	13620
ggctcggaaca	ggagagcgca	cgagggagct	tccaggggga	aacgcctggt	atctttatag	13680
tctgtcggg	tttcgccacc	tctgacttga	cgctcgattt	ttgtgatgct	cgtcaggggg	13740
gcgggacct	tggaaaaacg	ccagcaacgc	ggccttttta	cggttctctg	ccttttgctg	13800
cgccgcgtgc	ggctgctgga	gatggcggac	gcgatggata	tgttctgcca	agggttgggt	13860
tgcgcattca	cagttctccg	caagaattga	ttggctccaa	ttcttgaggt	ggtgaatccg	13920
ttagcgaggt	gccgcgggt	tccattcagg	tcgaggtggc	ccggctccat	gcaccgcgac	13980
gcaacgcggg	gaggcagaca	aggtataggg	cggcgcctac	aatccatgcc	aaccggttcc	14040
atgtgctcgc	cgaggcggca	taaatcgccg	tgacgatcag	cggctccagt	atcgaagtta	14100
ggctggttaag	agccgcgagc	gaccttgaa	gctgtccctg	atggtcgtca	tctacctgcc	14160
tggacagcat	ggcctgcaac	gcgggcatcc	cgatgccgc	ggaagcgaga	agaatcataa	14220
tggggaaggc	catccagcct	cgcgtcgcca	acgccagcaa	gacgtagccc	agcgcgtcgg	14280
ccgccatgcc	ctgcttcac	cccggtggcc	gttgctcgcg	tttgctggcg	gtgtccccgg	14340
aagaaatata	tttgcatgtc	tttagttcta	tgatgacaca	aaccccgccc	agcgtcttgt	14400
cattggcgaa	ttcgaacacg	cagatgcagt	cggggcggcg	cggctccagg	tccacttcgc	14460
atattaaggt	gacgcgtgtg	gcctcgaaca	ccgagcgacc	ctgcagcgac	cgccttaaca	14520
gcgtcaacag	cgtgccgcag	atcccgggca	atgagatatg	aaaaagcctg	aactcaccgc	14580
gacgtctgtc	gagaagtttc	tgatcgaaaa	gttcgacagc	gtctccgacc	tgatgcagct	14640
ctcggagggc	gaagaatctc	gtgctttcag	cttcgatgta	ggagggcgtg	gatatgtcct	14700
gcgggtaaat	agctgcgcgg	atggtttcta	caaagatcgt	tagtgggata	ggcactttgc	14760
atcggccggc	ctccccgatt	ccggaagtgc	ttgacattgg	ggaattcagc	gagagcctga	14820
cctattgcat	ctcccgccgt	gcacagggtg	tcacgttgca	agacctgcct	gaaaccgaac	14880
tgcccgctgt	tctgcagccg	gtcgcggagg	ccatggatgc	gatcgctgcg	gccgatctta	14940
gccagacgag	cgggttcggc	ccattcggac	cgcaaggaa	cggccaatac	actacatggc	15000
gtgatttcat	atgcgcgatt	gctgatcccc	atgtgtatca	ctggcaaact	gtgatggacg	15060
acaccgtcag	tgcgtccgtc	gcgcaggctc	tcgatgagct	gatgctttgg	gccgaggact	15120
gccccgaagt	ccggcacctc	gtgcacgcgg	atttcggctc	caacaatgtc	ctgacggaca	15180
atggccgcat	aacagcggtc	attgactgga	gcgaggcgat	gttcggggat	tccaataacg	15240
aggtcgcaa	catcttcttc	tggaggccgt	ggttggcggg	tatggagcag	cagacgcgct	15300
acttcgacg	gaggtatccg	gatcggcgag	gctccggcg	gctccggcg	tatatgctcc	15360
gcattggtct	tgaccaactc	tatcagagct	tggttgacgg	caatttcgat	gatgcagctt	15420
gggcgcaggg	tcgatgcgac	gcaatcgctc	gatccggagc	cgggactgtc	gggcgtacac	15480
aaatcgccc	cagaagcgcg	gccgtctgga	ccgatggctg	tgtagaagta	ctcgccgata	15540
gtggaaacgg	gagatggggg	aggctaactg	aaacacggaa	ggagacaata	ccggaaggaa	15600

cccgcgctat	gacggcaata	aaaagacaga	ataaaacgca	cgggtggttg	gtcgtttggt	15660
cataaacgcg	gggttcggtc	ccagggctgg	cactctgtcg	ataccccacc	gagaccccat	15720
tggggccaat	acgcccgcgt	tttttctttt	tccccacccc	accccccaag	ttcgggtgaa	15780
ggcccagggc	tcgcagccaa	cgtcggggcg	gcaggccctg	ccatagccac	tggccccgtg	15840
ggttagggac	ggggtcccc	atggggaatg	gtttatggtt	cgtggggggt	attatttttg	15900
gcgttgcggtg	gggtctggtc	cacgactgga	ctgagcagac	agacccatgg	tttttggtatg	15960
gcctgggcat	ggaccgcatg	tactggcgcg	acacgaacac	cgggcgtctg	tggctgccaa	16020
acacccccga	cccccaaaaa	ccaccgcgcg	gattttctggc	gtgccaagct	agtcgaccaa	16080

<210> 49  
 <211> 32  
 <212> DNA  
 <213> Homo sapiens

<400> 49  
 cccggccgga ggggcagctt tgtggagatg gt 32

<210> 50  
 <211> 11  
 <212> PRT  
 <213> Homo sapiens

<400> 50  
 Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val  
 1 5 10

<210> 51  
 <211> 5  
 <212> PRT  
 <213> Homo sapiens

<400> 51  
 Val Asn Leu Asp Ala  
 1 5

<210> 52  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligopeptide substrate

<400> 52  
 Ser Glu Val Asn Leu Asp Ala Glu Phe  
 1 5

<210> 53  
 <211> 30  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligopeptide substrate

<400> 53  
 Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile  
 1 5 10 15

Lys Thr Glu Glu Ile Ser Glu Val Asn Leu Asp Ala Glu Phe  
20 25 30

<210> 54  
<211> 5  
<212> PRT  
<213> Homo sapiens

<220>  
<223> Wild type Amyloid Precursor Protein cleavage site  
(fragment)

<400> 54  
Val Lys Met Asp Ala  
1 5

<210> 55  
<211> 24  
<212> PRT  
<213> Homo sapiens

<400> 55  
Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val  
1 5 10 15  
Glu Met Val Asp Asn Leu Arg Gly  
20

<210> 56  
<211> 15  
<212> PRT  
<213> Homo sapiens

<400> 56  
Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu Phe Arg  
1 5 10 15

<210> 57  
<211> 419  
<212> PRT  
<213> Homo sapiens

<400> 57  
Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val  
1 5 10 15  
Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser  
20 25 30  
Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp  
35 40 45  
Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val  
50 55 60  
Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr  
65 70 75 80  
Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser  
85 90 95  
Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr  
100 105 110  
Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val  
115 120 125  
Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp  
130 135 140  
Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile

145		150		155		160									
Ala	Ala	Ile	Thr	Glu	Ser	Asp	Lys	Phe	Phe	Ile	Asn	Gly	Ser	Asn	Trp
		165							170					175	
Glu	Gly	Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Glu	Ile	Ala	Arg	Pro	Asp	Asp
		180						185					190		
Ser	Leu	Glu	Pro	Phe	Phe	Asp	Ser	Leu	Val	Lys	Gln	Thr	His	Val	Pro
		195					200					205			
Asn	Leu	Phe	Ser	Leu	Gln	Leu	Cys	Gly	Ala	Gly	Phe	Pro	Leu	Asn	Gln
	210				215						220				
Ser	Glu	Val	Leu	Ala	Ser	Val	Gly	Gly	Ser	Met	Ile	Ile	Gly	Gly	Ile
225					230					235					240
Asp	His	Ser	Leu	Tyr	Thr	Gly	Ser	Leu	Trp	Tyr	Thr	Pro	Ile	Arg	Arg
			245						250					255	
Glu	Trp	Tyr	Tyr	Glu	Val	Ile	Ile	Val	Arg	Val	Glu	Ile	Asn	Gly	Gln
			260					265					270		
Asp	Leu	Lys	Met	Asp	Cys	Lys	Glu	Tyr	Asn	Tyr	Asp	Lys	Ser	Ile	Val
		275					280					285			
Asp	Ser	Gly	Thr	Thr	Asn	Leu	Arg	Leu	Pro	Lys	Lys	Val	Phe	Glu	Ala
	290				295						300				
Ala	Val	Lys	Ser	Ile	Lys	Ala	Ala	Ser	Ser	Thr	Glu	Lys	Phe	Pro	Asp
305					310					315					320
Gly	Phe	Trp	Leu	Gly	Glu	Gln	Leu	Val	Cys	Trp	Gln	Ala	Gly	Thr	Thr
			325						330					335	
Pro	Trp	Asn	Ile	Phe	Pro	Val	Ile	Ser	Leu	Tyr	Leu	Met	Gly	Glu	Val
			340					345					350		
Thr	Asn	Gln	Ser	Phe	Arg	Ile	Thr	Ile	Leu	Pro	Gln	Gln	Tyr	Leu	Arg
		355					360					365			
Pro	Val	Glu	Asp	Val	Ala	Thr	Ser	Gln	Asp	Asp	Cys	Tyr	Lys	Phe	Ala
	370				375						380				
Ile	Ser	Gln	Ser	Ser	Thr	Gly	Thr	Val	Met	Gly	Ala	Val	Ile	Met	Glu
385					390					395					400
Gly	Phe	Tyr	Val	Val	Phe	Asp	Arg	Ala	Arg	Lys	Arg	Ile	Gly	Phe	Ala
				405				410						415	
Val	Ser	Ala													

<210> 58  
 <211> 407  
 <212> PRT  
 <213> Homo sapiens

<400> 58

Glu	Thr	Asp	Glu	Glu	Pro	Glu	Glu	Pro	Gly	Arg	Arg	Gly	Ser	Phe	Val
1			5						10					15	
Glu	Met	Val	Asp	Asn	Leu	Arg	Gly	Lys	Ser	Gly	Gln	Gly	Tyr	Val	
			20					25					30		
Glu	Met	Thr	Val	Gly	Ser	Pro	Pro	Gln	Thr	Leu	Asn	Ile	Leu	Val	Asp
			35				40					45			
Thr	Gly	Ser	Ser	Asn	Phe	Ala	Val	Gly	Ala	Ala	Pro	His	Pro	Phe	Leu
	50				55						60				
His	Arg	Tyr	Tyr	Gln	Arg	Gln	Leu	Ser	Ser	Thr	Tyr	Arg	Asp	Leu	Arg
65					70					75					80
Lys	Gly	Val	Tyr	Val	Pro	Tyr	Thr	Gln	Gly	Lys	Trp	Glu	Gly	Glu	Leu
				85					90					95	
Gly	Thr	Asp	Leu	Val	Ser	Ile	Pro	His	Gly	Pro	Asn	Val	Thr	Val	Arg
			100					105					110		
Ala	Asn	Ile	Ala	Ala	Ile	Thr	Glu	Ser	Asp	Lys	Phe	Phe	Ile	Asn	Gly
			115				120					125			
Ser	Asn	Trp	Glu	Gly	Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Glu	Ile	Ala	Arg
	130					135					140				
Pro	Asp	Asp	Ser	Leu	Glu	Pro	Phe	Phe	Asp	Ser	Leu	Val	Lys	Gln	Thr

145					150					155				160
His	Val	Pro	Asn	Leu	Phe	Ser	Leu	Gln	Leu	Cys	Gly	Ala	Gly	Phe
				165					170					175
Leu	Asn	Gln	Ser	Glu	Val	Leu	Ala	Ser	Val	Gly	Gly	Ser	Met	Ile
			180					185					190	
Gly	Gly	Ile	Asp	His	Ser	Leu	Tyr	Thr	Gly	Ser	Leu	Trp	Tyr	Thr
		195					200					205		Pro
Ile	Arg	Arg	Glu	Trp	Tyr	Tyr	Glu	Val	Ile	Ile	Val	Arg	Val	Glu
	210				215						220			Ile
Asn	Gly	Gln	Asp	Leu	Lys	Met	Asp	Cys	Lys	Glu	Tyr	Asn	Tyr	Asp
225					230					235				240
Ser	Ile	Val	Asp	Ser	Gly	Thr	Thr	Asn	Leu	Arg	Leu	Pro	Lys	Lys
			245					250						255
Phe	Glu	Ala	Ala	Val	Lys	Ser	Ile	Lys	Ala	Ala	Ser	Ser	Thr	Glu
			260					265					270	Lys
Phe	Pro	Asp	Gly	Phe	Trp	Leu	Gly	Glu	Gln	Leu	Val	Cys	Trp	Gln
		275					280					285		Ala
Gly	Thr	Thr	Pro	Trp	Asn	Ile	Phe	Pro	Val	Ile	Ser	Leu	Tyr	Leu
	290				295						300			Met
Gly	Glu	Val	Thr	Asn	Gln	Ser	Phe	Arg	Ile	Thr	Ile	Leu	Pro	Gln
305				310					315					320
Tyr	Leu	Arg	Pro	Val	Glu	Asp	Val	Ala	Thr	Ser	Gln	Asp	Asp	Cys
			325					330						335
Lys	Phe	Ala	Ile	Ser	Gln	Ser	Ser	Thr	Gly	Thr	Val	Met	Gly	Ala
		340						345				350		Val
Ile	Met	Glu	Gly	Phe	Tyr	Val	Val	Phe	Asp	Arg	Ala	Arg	Lys	Arg
	355					360					365			Ile
Gly	Phe	Ala	Val	Ser	Ala	Cys	His	Val	His	Asp	Glu	Phe	Arg	Thr
	370				375					380				Ala
Ala	Val	Glu	Gly	Pro	Phe	Val	Thr	Leu	Asp	Met	Glu	Asp	Cys	Gly
385				390					395					400
Asn	Ile	Pro	Gln	Thr	Asp	Glu								
				405										

<210> 59  
 <211> 452  
 <212> PRT  
 <213> Homo sapiens

<400> 59

Met	Ala	Gln	Ala	Leu	Pro	Trp	Leu	Leu	Leu	Trp	Met	Gly	Ala	Gly	Val
1				5					10					15	
Leu	Pro	Ala	His	Gly	Thr	Gln	His	Gly	Ile	Arg	Leu	Pro	Leu	Arg	Ser
			20					25					30		
Gly	Leu	Gly	Gly	Ala	Pro	Leu	Gly	Leu	Arg	Leu	Pro	Arg	Glu	Thr	Asp
	35					40					45				
Glu	Glu	Pro	Glu	Glu	Pro	Gly	Arg	Arg	Gly	Ser	Phe	Val	Glu	Met	Val
	50				55					60					
Asp	Asn	Leu	Arg	Gly	Lys	Ser	Gly	Gln	Gly	Tyr	Tyr	Val	Glu	Met	Thr
65			70						75					80	
Val	Gly	Ser	Pro	Pro	Gln	Thr	Leu	Asn	Ile	Leu	Val	Asp	Thr	Gly	Ser
			85					90						95	
Ser	Asn	Phe	Ala	Val	Gly	Ala	Ala	Pro	His	Pro	Phe	Leu	His	Arg	Tyr
	100						105					110			
Tyr	Gln	Arg	Gln	Leu	Ser	Ser	Thr	Tyr	Arg	Asp	Leu	Arg	Lys	Gly	Val
	115					120					125				
Tyr	Val	Pro	Tyr	Thr	Gln	Gly	Lys	Trp	Glu	Gly	Glu	Leu	Gly	Thr	Asp
	130				135					140					
Leu	Val	Ser	Ile	Pro	His	Gly	Pro	Asn	Val	Thr	Val	Arg	Ala	Asn	Ile
145				150					155					160	
Ala	Ala	Ile	Thr	Glu	Ser	Asp	Lys	Phe	Phe	Ile	Asn	Gly	Ser	Asn	Trp



130		135		140
Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile				
145		150		155
Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp				
	165		170	175
Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp				
	180		185	190
Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro				
	195		200	205
Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln				
	210		215	220
Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile				
225		230		235
Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg				
	245		250	255
Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln				
	260		265	270
Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val				
	275		280	285
Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala				
	290		295	300
Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp				
305		310		315
Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr				
	325		330	335
Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val				
	340		345	350
Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg				
	355		360	365
Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala				
	370		375	380
Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu				
385		390		395
Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala				
	405		410	415
Val Ser Ala Cys				
	420			

<210> 61

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic peptide inhibitor

<221> MOD\_RES

<222> 4

<223> Xaa = hydroxyethylene

<400> 61

Glu Val Met Xaa Ala Glu Phe

1

5

<210> 62

<211> 26

<212> PRT

<213> Homo sapiens

<400> 62

Leu Met Thr Ile Ala Tyr Val Met Ala Ala Ile Cys Ala Leu Phe Met



1	5	10	15
Leu	Pro	Leu	Cys
20	Leu	Met	Val
	Cys	Gln	Trp
	25		

<210> 63  
 <211> 33  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> P26-P4'sw peptide substrate

<400> 63  
 Cys Gly Gly Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser Gly Leu  
 1 5 10 15  
 Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Asn Leu Asp Ala Glu  
 20 25 30  
 Phe

<210> 64  
 <211> 29  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> P26-P1' peptide substrate with CGG linker

<400> 64  
 Cys Gly Gly Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser Gly Leu  
 1 5 10 15  
 Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Asn Leu  
 20 25

<210> 65  
 <211> 501  
 <212> PRT  
 <213> Mus musculus

<400> 65  
 Met Ala Pro Ala Leu His Trp Leu Leu Leu Trp Val Gly Ser Gly Met  
 1 5 10 15  
 Leu Pro Ala Gln Gly Thr His Leu Gly Ile Arg Leu Pro Leu Arg Ser  
 20 25 30  
 Gly Leu Ala Gly Pro Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp  
 35 40 45  
 Glu Glu Ser Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val  
 50 55 60  
 Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr  
 65 70 75 80  
 Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser  
 85 90 95  
 Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr  
 100 105 110  
 Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val  
 115 120 125  
 Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp  
 130 135 140  
 Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile  
 145 150 155 160  
 Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp



				85					90					95			
Ser	Ser	Thr	Tyr	Arg	Asp	Leu	Arg	Lys	Gly	Val	Tyr	Val	Pro	Tyr	Thr		
			100					105					110				
Gln	Gly	Lys	Trp	Glu	Gly	Glu	Leu	Gly	Thr	Asp	Leu	Val	Ser	Ile	Pro		
		115					120					125					
His	Gly	Pro	Asn	Val	Thr	Val	Arg	Ala	Asn	Ile	Ala	Ala	Ile	Thr	Glu		
	130					135					140						
Ser	Asp	Lys	Phe	Phe	Ile	Asn	Gly	Ser	Asn	Trp	Glu	Gly	Ile	Leu	Gly		
145					150					155				160			
Leu	Ala	Tyr	Ala	Glu	Ile	Ala	Arg	Pro	Asp	Asp	Ser	Leu	Glu	Pro	Phe		
			165						170					175			
Phe	Asp	Ser	Leu	Val	Lys	Gln	Thr	His	Val	Pro	Asn	Leu	Phe	Ser	Leu		
		180						185					190				
Gln	Leu	Cys	Gly	Ala	Gly	Phe	Pro	Leu	Asn	Gln	Ser	Glu	Val	Leu	Ala		
		195					200					205					
Ser	Val	Gly	Gly	Ser	Met	Ile	Ile	Gly	Gly	Ile	Asp	His	Ser	Leu	Tyr		
	210				215						220						
Thr	Gly	Ser	Leu	Trp	Tyr	Thr	Pro	Ile	Arg	Arg	Glu	Trp	Tyr	Tyr	Glu		
225					230					235					240		
Val	Ile	Ile	Val	Arg	Val	Glu	Ile	Asn	Gly	Gln	Asp	Leu	Lys	Met	Asp		
			245						250					255			
Cys	Lys	Glu	Tyr	Asn	Tyr	Asp	Lys	Ser	Ile	Val	Asp	Ser	Gly	Thr	Thr		
		260						265					270				
Asn	Leu	Arg	Leu	Pro	Lys	Lys	Val	Phe	Glu	Ala	Ala	Val	Lys	Ser	Ile		
		275					280					285					
Lys	Ala	Ala	Ser	Ser	Thr	Glu	Lys	Phe	Pro	Asp	Gly	Phe	Trp	Leu	Gly		
	290				295						300						
Glu	Gln	Leu	Val	Cys	Trp	Gln	Ala	Gly	Thr	Thr	Pro	Trp	Asn	Ile	Phe		
305					310					315					320		
Pro	Val	Ile	Ser	Leu	Tyr	Leu	Met	Gly	Glu	Val	Thr	Asn	Gln	Ser	Phe		
			325					330						335			
Arg	Ile	Thr	Ile	Leu	Pro	Gln	Gln	Tyr	Leu	Arg	Pro	Val	Glu	Asp	Val		
			340					345					350				
Ala	Thr	Ser	Gln	Asp	Asp	Cys	Tyr	Lys	Phe	Ala	Ile	Ser	Gln	Ser	Ser		
		355				360						365					
Thr	Gly	Thr	Val	Met	Gly	Ala	Val	Ile	Met	Glu	Gly	Phe	Tyr	Val	Val		
	370				375						380						
Phe	Asp	Arg	Ala	Arg	Lys	Arg	Ile	Gly	Phe	Ala	Val	Ser	Ala	Cys	His		
385					390					395					400		
Val	His	Asp	Glu	Phe	Arg	Thr	Ala	Ala	Val	Glu	Gly	Pro	Phe	Val	Thr		
			405						410					415			
Leu	Asp	Met	Glu	Asp	Cys	Gly	Tyr	Asn	Ile	Pro	Gln	Thr	Asp	Glu	Ser		
		420						425					430				
Thr	Leu	Met	Thr	Ile	Ala	Tyr	Val	Met	Ala	Ala	Ile	Cys	Ala	Leu	Phe		
		435					440					445					
Met	Leu	Pro	Leu	Cys	Leu	Met	Val	Cys	Gln	Trp	Arg	Cys	Leu	Arg	Cys		
	450					455					460						
Leu	Arg	Gln	Gln	His	Asp	Asp	Phe	Ala	Asp	Asp	Ile	Ser	Leu	Leu	Lys		
465					470					475					480		

<210> 67

<211> 444

<212> PRT

<213> Homo sapiens

<400> 67

Gly	Ser	Phe	Val	Glu	Met	Val	Asp	Asn	Leu	Arg	Gly	Lys	Ser	Gly	Gln		
1				5					10					15			
Gly	Tyr	Tyr	Val	Glu	Met	Thr	Val	Gly	Ser	Pro	Pro	Gln	Thr	Leu	Asn		
			20					25					30				

Ile	Leu	Val	Asp	Thr	Gly	Ser	Ser	Asn	Phe	Ala	Val	Gly	Ala	Ala	Pro
		35					40					45			
His	Pro	Phe	Leu	His	Arg	Tyr	Tyr	Gln	Arg	Gln	Leu	Ser	Ser	Thr	Tyr
	50					55					60				
Arg	Asp	Leu	Arg	Lys	Gly	Val	Tyr	Val	Pro	Tyr	Thr	Gln	Gly	Lys	Trp
65					70				75						80
Glu	Gly	Glu	Leu	Gly	Thr	Asp	Leu	Val	Ser	Ile	Pro	His	Gly	Pro	Asn
				85					90					95	
Val	Thr	Val	Arg	Ala	Asn	Ile	Ala	Ala	Ile	Thr	Glu	Ser	Asp	Lys	Phe
			100					105					110		
Phe	Ile	Asn	Gly	Ser	Asn	Trp	Glu	Gly	Ile	Leu	Gly	Leu	Ala	Tyr	Ala
		115					120					125			
Glu	Ile	Ala	Arg	Pro	Asp	Asp	Ser	Leu	Glu	Pro	Phe	Phe	Asp	Ser	Leu
	130					135					140				
Val	Lys	Gln	Thr	His	Val	Pro	Asn	Leu	Phe	Ser	Leu	Gln	Leu	Cys	Gly
145					150					155					160
Ala	Gly	Phe	Pro	Leu	Asn	Gln	Ser	Glu	Val	Leu	Ala	Ser	Val	Gly	Gly
				165					170					175	
Ser	Met	Ile	Ile	Gly	Gly	Ile	Asp	His	Ser	Leu	Tyr	Thr	Gly	Ser	Leu
		180						185					190		
Trp	Tyr	Thr	Pro	Ile	Arg	Arg	Glu	Trp	Tyr	Tyr	Glu	Val	Ile	Ile	Val
		195					200					205			
Arg	Val	Glu	Ile	Asn	Gly	Gln	Asp	Leu	Lys	Met	Asp	Cys	Lys	Glu	Tyr
	210					215					220				
Asn	Tyr	Asp	Lys	Ser	Ile	Val	Asp	Ser	Gly	Thr	Thr	Asn	Leu	Arg	Leu
225					230					235					240
Pro	Lys	Lys	Val	Phe	Glu	Ala	Ala	Val	Lys	Ser	Ile	Lys	Ala	Ala	Ser
				245					250					255	
Ser	Thr	Glu	Lys	Phe	Pro	Asp	Gly	Phe	Trp	Leu	Gly	Glu	Gln	Leu	Val
			260					265					270		
Cys	Trp	Gln	Ala	Gly	Thr	Thr	Pro	Trp	Asn	Ile	Phe	Pro	Val	Ile	Ser
		275					280					285			
Leu	Tyr	Leu	Met	Gly	Glu	Val	Thr	Asn	Gln	Ser	Phe	Arg	Ile	Thr	Ile
	290					295					300				
Leu	Pro	Gln	Gln	Tyr	Leu	Arg	Pro	Val	Glu	Asp	Val	Ala	Thr	Ser	Gln
305					310					315					320
Asp	Asp	Cys	Tyr	Lys	Phe	Ala	Ile	Ser	Gln	Ser	Ser	Thr	Gly	Thr	Val
				325					330					335	
Met	Gly	Ala	Val	Ile	Met	Glu	Gly	Phe	Tyr	Val	Val	Phe	Asp	Arg	Ala
			340					345					350		
Arg	Lys	Arg	Ile	Gly	Phe	Ala	Val	Ser	Ala	Cys	His	Val	His	Asp	Glu
		355					360					365			
Phe	Arg	Thr	Ala	Ala	Val	Glu	Gly	Pro	Phe	Val	Thr	Leu	Asp	Met	Glu
	370					375					380				
Asp	Cys	Gly	Tyr	Asn	Ile	Pro	Gln	Thr	Asp	Glu	Ser	Thr	Leu	Met	Thr
385					390					395					400
Ile	Ala	Tyr	Val	Met	Ala	Ala	Ile	Cys	Ala	Leu	Phe	Met	Leu	Pro	Leu
				405					410					415	
Cys	Leu	Met	Val	Cys	Gln	Trp	Arg	Cys	Leu	Arg	Cys	Leu	Arg	Gln	Gln
			420					425					430		
His	Asp	Asp	Phe	Ala	Asp	Asp	Ile	Ser	Leu	Leu	Lys				
		435					440								

<210> 68

<211> 395

<212> PRT

<213> Homo sapiens

<400> 68

Gly	Ser	Phe	Val	Glu	Met	Val	Asp	Asn	Leu	Arg	Gly	Lys	Ser	Gly	Gln
1				5					10					15	

Gly Tyr Tyr Val Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn  
 20 25 30  
 Ile Leu Val Asp Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro  
 35 40 45  
 His Pro Phe Leu His Arg Tyr Tyr Gln Arg Gln Leu Ser Ser Thr Tyr  
 50 55 60  
 Arg Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr Thr Gln Gly Lys Trp  
 65 70 75 80  
 Glu Gly Glu Leu Gly Thr Asp Leu Val Ser Ile Pro His Gly Pro Asn  
 85 90 95  
 Val Thr Val Arg Ala Asn Ile Ala Ala Ile Thr Glu Ser Asp Lys Phe  
 100 105 110  
 Phe Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu Gly Leu Ala Tyr Ala  
 115 120 125  
 Glu Ile Ala Arg Pro Asp Asp Ser Leu Glu Pro Phe Phe Asp Ser Leu  
 130 135 140  
 Val Lys Gln Thr His Val Pro Asn Leu Phe Ser Leu Gln Leu Cys Gly  
 145 150 155 160  
 Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala Ser Val Gly Gly  
 165 170 175  
 Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr Thr Gly Ser Leu  
 180 185 190  
 Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu Val Ile Ile Val  
 195 200 205  
 Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp Cys Lys Glu Tyr  
 210 215 220  
 Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr Asn Leu Arg Leu  
 225 230 235 240  
 Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile Lys Ala Ala Ser  
 245 250 255  
 Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly Glu Gln Leu Val  
 260 265 270  
 Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe Pro Val Ile Ser  
 275 280 285  
 Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe Arg Ile Thr Ile  
 290 295 300  
 Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val Ala Thr Ser Gln  
 305 310 315 320  
 Asp Asp Cys Tyr Lys Phe Ala Ile Ser Gln Ser Ser Thr Gly Thr Val  
 325 330 335  
 Met Gly Ala Val Ile Met Glu Gly Phe Tyr Val Val Phe Asp Arg Ala  
 340 345 350  
 Arg Lys Arg Ile Gly Phe Ala Val Ser Ala Cys His Val His Asp Glu  
 355 360 365  
 Phe Arg Thr Ala Ala Val Glu Gly Pro Phe Val Thr Leu Asp Met Glu  
 370 375 380  
 Asp Cys Gly Tyr Asn Ile Pro Gln Thr Asp Glu  
 385 390 395

<210> 69

<211> 439

<212> PRT

<213> Homo sapiens

<400> 69

Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu  
 1 5 10 15  
 Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr  
 20 25 30  
 Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His  
 35 40 45

Arg	Tyr	Tyr	Gln	Arg	Gln	Leu	Ser	Ser	Thr	Tyr	Arg	Asp	Leu	Arg	Lys
50						55					60				
Gly	Val	Tyr	Val	Pro	Tyr	Thr	Gln	Gly	Lys	Trp	Glu	Gly	Glu	Leu	Gly
65					70					75					80
Thr	Asp	Leu	Val	Ser	Ile	Pro	His	Gly	Pro	Asn	Val	Thr	Val	Arg	Ala
				85					90					95	
Asn	Ile	Ala	Ala	Ile	Thr	Glu	Ser	Asp	Lys	Phe	Phe	Ile	Asn	Gly	Ser
		100						105					110		
Asn	Trp	Glu	Gly	Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Glu	Ile	Ala	Arg	Pro
	115					120							125		
Asp	Asp	Ser	Leu	Glu	Pro	Phe	Phe	Asp	Ser	Leu	Val	Lys	Gln	Thr	His
	130					135						140			
Val	Pro	Asn	Leu	Phe	Ser	Leu	Gln	Leu	Cys	Gly	Ala	Gly	Phe	Pro	Leu
145				150						155					160
Asn	Gln	Ser	Glu	Val	Leu	Ala	Ser	Val	Gly	Gly	Ser	Met	Ile	Ile	Gly
			165						170					175	
Gly	Ile	Asp	His	Ser	Leu	Tyr	Thr	Gly	Ser	Leu	Trp	Tyr	Thr	Pro	Ile
		180						185						190	
Arg	Arg	Glu	Trp	Tyr	Tyr	Glu	Val	Ile	Ile	Val	Arg	Val	Glu	Ile	Asn
		195					200						205		
Gly	Gln	Asp	Leu	Lys	Met	Asp	Cys	Lys	Glu	Tyr	Asn	Tyr	Asp	Lys	Ser
	210					215						220			
Ile	Val	Asp	Ser	Gly	Thr	Thr	Asn	Leu	Arg	Leu	Pro	Lys	Lys	Val	Phe
225					230					235					240
Glu	Ala	Ala	Val	Lys	Ser	Ile	Lys	Ala	Ala	Ser	Ser	Thr	Glu	Lys	Phe
				245					250					255	
Pro	Asp	Gly	Phe	Trp	Leu	Gly	Glu	Gln	Leu	Val	Cys	Trp	Gln	Ala	Gly
			260					265						270	
Thr	Thr	Pro	Trp	Asn	Ile	Phe	Pro	Val	Ile	Ser	Leu	Tyr	Leu	Met	Gly
		275					280						285		
Glu	Val	Thr	Asn	Gln	Ser	Phe	Arg	Ile	Thr	Ile	Leu	Pro	Gln	Gln	Tyr
	290					295					300				
Leu	Arg	Pro	Val	Glu	Asp	Val	Ala	Thr	Ser	Gln	Asp	Asp	Cys	Tyr	Lys
305					310					315					320
Phe	Ala	Ile	Ser	Gln	Ser	Ser	Thr	Gly	Thr	Val	Met	Gly	Ala	Val	Ile
				325					330					335	
Met	Glu	Gly	Phe	Tyr	Val	Val	Phe	Asp	Arg	Ala	Arg	Lys	Arg	Ile	Gly
			340					345					350		
Phe	Ala	Val	Ser	Ala	Cys	His	Val	His	Asp	Glu	Phe	Arg	Thr	Ala	Ala
		355					360					365			
Val	Glu	Gly	Pro	Phe	Val	Thr	Leu	Asp	Met	Glu	Asp	Cys	Gly	Tyr	Asn
	370					375						380			
Ile	Pro	Gln	Thr	Asp	Glu	Ser	Thr	Leu	Met	Thr	Ile	Ala	Tyr	Val	Met
385					390					395					400
Ala	Ala	Ile	Cys	Ala	Leu	Phe	Met	Leu	Pro	Leu	Cys	Leu	Met	Val	Cys
				405					410					415	
Gln	Trp	Arg	Cys	Leu	Arg	Cys	Leu	Arg	Gln	Gln	His	Asp	Asp	Phe	Ala
			420					425					430		
Asp	Asp	Ile	Ser	Leu	Leu	Lys									
		435													


<210> 70  
 <211> 390  
 <212> PRT  
 <213> Homo sapiens

<400> 70  
 Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu  
 1 5 10 15  
 Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr  
 20 25 30

Gly	Ser	Ser	Asn	Phe	Ala	Val	Gly	Ala	Ala	Pro	His	Pro	Phe	Leu	His
		35					40					45			
Arg	Tyr	Tyr	Gln	Arg	Gln	Leu	Ser	Ser	Thr	Tyr	Arg	Asp	Leu	Arg	Lys
	50					55					60				
Gly	Val	Tyr	Val	Pro	Tyr	Thr	Gln	Gly	Lys	Trp	Glu	Gly	Glu	Leu	Gly
65					70					75					80
Thr	Asp	Leu	Val	Ser	Ile	Pro	His	Gly	Pro	Asn	Val	Thr	Val	Arg	Ala
				85					90					95	
Asn	Ile	Ala	Ala	Ile	Thr	Glu	Ser	Asp	Lys	Phe	Phe	Ile	Asn	Gly	Ser
			100						105				110		
Asn	Trp	Glu	Gly	Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Glu	Ile	Ala	Arg	Pro
		115				120						125			
Asp	Asp	Ser	Leu	Glu	Pro	Phe	Phe	Asp	Ser	Leu	Val	Lys	Gln	Thr	His
	130					135					140				
Val	Pro	Asn	Leu	Phe	Ser	Leu	Gln	Leu	Cys	Gly	Ala	Gly	Phe	Pro	Leu
145					150					155					160
Asn	Gln	Ser	Glu	Val	Leu	Ala	Ser	Val	Gly	Gly	Ser	Met	Ile	Ile	Gly
				165					170					175	
Gly	Ile	Asp	His	Ser	Leu	Tyr	Thr	Gly	Ser	Leu	Trp	Tyr	Thr	Pro	Ile
			180					185					190		
Arg	Arg	Glu	Trp	Tyr	Tyr	Glu	Val	Ile	Ile	Val	Arg	Val	Glu	Ile	Asn
		195				200						205			
Gly	Gln	Asp	Leu	Lys	Met	Asp	Cys	Lys	Glu	Tyr	Asn	Tyr	Asp	Lys	Ser
	210					215					220				
Ile	Val	Asp	Ser	Gly	Thr	Thr	Asn	Leu	Arg	Leu	Pro	Lys	Lys	Val	Phe
225					230					235					240
Glu	Ala	Ala	Val	Lys	Ser	Ile	Lys	Ala	Ala	Ser	Ser	Thr	Glu	Lys	Phe
				245					250					255	
Pro	Asp	Gly	Phe	Trp	Leu	Gly	Glu	Gln	Leu	Val	Cys	Trp	Gln	Ala	Gly
			260					265					270		
Thr	Thr	Pro	Trp	Asn	Ile	Phe	Pro	Val	Ile	Ser	Leu	Tyr	Leu	Met	Gly
		275				280						285			
Glu	Val	Thr	Asn	Gln	Ser	Phe	Arg	Ile	Thr	Ile	Leu	Pro	Gln	Gln	Tyr
	290					295					300				
Leu	Arg	Pro	Val	Glu	Asp	Val	Ala	Thr	Ser	Gln	Asp	Asp	Cys	Tyr	Lys
305					310					315					320
Phe	Ala	Ile	Ser	Gln	Ser	Ser	Thr	Gly	Thr	Val	Met	Gly	Ala	Val	Ile
				325					330					335	
Met	Glu	Gly	Phe	Tyr	Val	Val	Phe	Asp	Arg	Ala	Arg	Lys	Arg	Ile	Gly
			340					345					350		
Phe	Ala	Val	Ser	Ala	Cys	His	Val	His	Asp	Glu	Phe	Arg	Thr	Ala	Ala
		355					360					365			
Val	Glu	Gly	Pro	Phe	Val	Thr	Leu	Asp	Met	Glu	Asp	Cys	Gly	Tyr	Asn
	370					375					380				
Ile	Pro	Gln	Thr	Asp	Glu										
385					390										

<210> 71  
 <211> 374  
 <212> PRT  
 <213> Homo sapiens

<400> 71  
 Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val  
 1 5 10 15  
 Glu Met Val Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val  
 20 25 30  
 Glu Met Thr Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp  
 35 40 45  
 Thr Gly Ser Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu  
 50 55 60



His	Arg	Tyr	Tyr	Gln	Arg	Gln	Leu	Ser	Ser	Thr	Tyr	Arg	Asp	Leu	Arg
65					70					75					80
Lys	Gly	Val	Tyr	Val	Pro	Tyr	Thr	Gln	Gly	Lys	Trp	Glu	Gly	Glu	Leu
				85					90					95	
Gly	Thr	Asp	Leu	Val	Ser	Ile	Pro	His	Gly	Pro	Asn	Val	Thr	Val	Arg
			100					105					110		
Ala	Asn	Ile	Ala	Ala	Ile	Thr	Glu	Ser	Asp	Lys	Phe	Phe	Ile	Asn	Gly
		115					120					125			
Ser	Asn	Trp	Glu	Gly	Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Glu	Ile	Ala	Arg
	130					135					140				
Pro	Asp	Asp	Ser	Leu	Glu	Pro	Phe	Phe	Asp	Ser	Leu	Val	Lys	Gln	Thr
145					150					155					160
His	Val	Pro	Asn	Leu	Phe	Ser	Leu	Gln	Leu	Cys	Gly	Ala	Gly	Phe	Pro
			165					170						175	
Leu	Asn	Gln	Ser	Glu	Val	Leu	Ala	Ser	Val	Gly	Gly	Ser	Met	Ile	Ile
			180					185					190		
Gly	Gly	Ile	Asp	His	Ser	Leu	Tyr	Thr	Gly	Ser	Leu	Trp	Tyr	Thr	Pro
		195					200					205			
Ile	Arg	Arg	Glu	Trp	Tyr	Tyr	Glu	Val	Ile	Ile	Val	Arg	Val	Glu	Ile
	210					215					220				
Asn	Gly	Gln	Asp	Leu	Lys	Met	Asp	Cys	Lys	Glu	Tyr	Asn	Tyr	Asp	Lys
225					230					235					240
Ser	Ile	Val	Asp	Ser	Gly	Thr	Thr	Asn	Leu	Arg	Leu	Pro	Lys	Lys	Val
			245					250						255	
Phe	Glu	Ala	Ala	Val	Lys	Ser	Ile	Lys	Ala	Ala	Ser	Ser	Thr	Glu	Lys
		260						265					270		
Phe	Pro	Asp	Gly	Phe	Trp	Leu	Gly	Glu	Gln	Leu	Val	Cys	Trp	Gln	Ala
		275					280					285			
Gly	Thr	Thr	Pro	Trp	Asn	Ile	Phe	Pro	Val	Ile	Ser	Leu	Tyr	Leu	Met
	290					295					300				
Gly	Glu	Val	Thr	Asn	Gln	Ser	Phe	Arg	Ile	Thr	Ile	Leu	Pro	Gln	Gln
305					310					315					320
Tyr	Leu	Arg	Pro	Val	Glu	Asp	Val	Ala	Thr	Ser	Gln	Asp	Asp	Cys	Tyr
			325					330						335	
Lys	Phe	Ala	Ile	Ser	Gln	Ser	Ser	Thr	Gly	Thr	Val	Met	Gly	Ala	Val
		340						345					350		
Ile	Met	Glu	Gly	Phe	Tyr	Val	Val	Phe	Asp	Arg	Ala	Arg	Lys	Arg	Ile
		355				360						365			
Gly	Phe	Ala	Val	Ser	Ala										
		370													

<210> 72

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> P10-P4'staD-V peptide inhibitor

<221> MOD\_RES

<222> 10

<223> Xaa is statine moiety

<400> 72

Lys	Thr	Glu	Glu	Ile	Ser	Glu	Val	Asn	Xaa	Val	Ala	Glu	Phe
1				5					10				

<210> 73

<211> 9

<212> PRT

<213> Artificial Sequence



<220>  
<223> P4-P4'staD-V peptide inhibitor

<221> MOD\_RES  
<222> 5  
<223> Xaa is statine moiety

<400> 73  
Ser Glu Val Asn Xaa Val Ala Glu Phe  
1 5

<210> 74  
<211> 431  
<212> PRT  
<213> Homo sapiens

<400> 74  
Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser Gly Leu Gly Gly Ala  
1 5 10 15  
Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp Glu Glu Pro Glu Glu  
20 25 30  
Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val Asp Asn Leu Arg Gly  
35 40 45  
Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr Val Gly Ser Pro Pro  
50 55 60  
Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser Ser Asn Phe Ala Val  
65 70 75 80  
Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr Tyr Gln Arg Gln Leu  
85 90 95  
Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val Tyr Val Pro Tyr Thr  
100 105 110  
Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp Leu Val Ser Ile Pro  
115 120 125  
His Gly Pro Asn Val Thr Val Arg Ala Asn Ile Ala Ala Ile Thr Glu  
130 135 140  
Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp Glu Gly Ile Leu Gly  
145 150 155 160  
Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp Ser Leu Glu Pro Phe  
165 170 175  
Phe Asp Ser Leu Val Lys Gln Thr His Val Pro Asn Leu Phe Ser Leu  
180 185 190  
Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln Ser Glu Val Leu Ala  
195 200 205  
Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile Asp His Ser Leu Tyr  
210 215 220  
Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg Glu Trp Tyr Tyr Glu  
225 230 235 240  
Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln Asp Leu Lys Met Asp  
245 250 255  
Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val Asp Ser Gly Thr Thr  
260 265 270  
Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala Ala Val Lys Ser Ile  
275 280 285  
Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp Gly Phe Trp Leu Gly  
290 295 300  
Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr Pro Trp Asn Ile Phe  
305 310 315 320  
Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val Thr Asn Gln Ser Phe  
325 330 335  
Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg Pro Val Glu Asp Val

Ala	Thr	Ser	340	Gln	Asp	Asp	Cys	Tyr	345	Lys	Phe	Ala	Ile	Ser	350	Gln	Ser	Ser
		355						360						365				
Thr	Gly	Thr	Val	Met	Gly	Ala	Val	Ile	Met	Glu	Gly	Phe	Tyr	Val	Val			
	370					375					380							
Phe	Asp	Arg	Ala	Arg	Lys	Arg	Ile	Gly	Phe	Ala	Val	Ser	Ala	Cys	His			
385					390					395					400			
Val	His	Asp	Glu	Phe	Arg	Thr	Ala	Ala	Val	Glu	Gly	Pro	Phe	Val	Thr			
			405						410					415				
Leu	Asp	Met	Glu	Asp	Cys	Gly	Tyr	Asn	Ile	Pro	Gln	Thr	Asp	Glu				
			420					425					430					

<210> 75  
 <211> 361  
 <212> PRT  
 <213> Homo sapiens

<400> 75

Met	Val	Asp	Asn	Leu	Arg	Gly	Lys	Ser	Gly	Gln	Gly	Tyr	Tyr	Val	Glu			
1			5						10					15				
Met	Thr	Val	Gly	Ser	Pro	Pro	Gln	Thr	Leu	Asn	Ile	Leu	Val	Asp	Thr			
		20					25						30					
Gly	Ser	Ser	Asn	Phe	Ala	Val	Gly	Ala	Ala	Pro	His	Pro	Phe	Leu	His			
	35						40					45						
Arg	Tyr	Tyr	Gln	Arg	Gln	Leu	Ser	Ser	Thr	Tyr	Arg	Asp	Leu	Arg	Lys			
	50					55					60							
Gly	Val	Tyr	Val	Pro	Tyr	Thr	Gln	Gly	Lys	Trp	Glu	Gly	Glu	Leu	Gly			
65					70					75				80				
Thr	Asp	Leu	Val	Ser	Ile	Pro	His	Gly	Pro	Asn	Val	Thr	Val	Arg	Ala			
			85					90					95					
Asn	Ile	Ala	Ala	Ile	Thr	Glu	Ser	Asp	Lys	Phe	Phe	Ile	Asn	Gly	Ser			
		100						105					110					
Asn	Trp	Glu	Gly	Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Glu	Ile	Ala	Arg	Pro			
	115					120						125						
Asp	Asp	Ser	Leu	Glu	Pro	Phe	Phe	Asp	Ser	Leu	Val	Lys	Gln	Thr	His			
	130					135					140							
Val	Pro	Asn	Leu	Phe	Ser	Leu	Gln	Leu	Cys	Gly	Ala	Gly	Phe	Pro	Leu			
145					150					155					160			
Asn	Gln	Ser	Glu	Val	Leu	Ala	Ser	Val	Gly	Gly	Ser	Met	Ile	Ile	Gly			
			165						170					175				
Gly	Ile	Asp	His	Ser	Leu	Tyr	Thr	Gly	Ser	Leu	Trp	Tyr	Thr	Pro	Ile			
		180						185					190					
Arg	Arg	Glu	Trp	Tyr	Tyr	Glu	Val	Ile	Ile	Val	Arg	Val	Glu	Ile	Asn			
	195					200						205						
Gly	Gln	Asp	Leu	Lys	Met	Asp	Cys	Lys	Glu	Tyr	Asn	Tyr	Asp	Lys	Ser			
	210					215					220							
Ile	Val	Asp	Ser	Gly	Thr	Asn	Leu	Arg	Leu	Pro	Lys	Lys	Val	Phe				
225					230				235					240				
Glu	Ala	Ala	Val	Lys	Ser	Ile	Lys	Ala	Ala	Ser	Ser	Thr	Glu	Lys	Phe			
			245					250					255					
Pro	Asp	Gly	Phe	Trp	Leu	Gly	Glu	Gln	Leu	Val	Cys	Trp	Gln	Ala	Gly			
		260						265					270					
Thr	Thr	Pro	Trp	Asn	Ile	Phe	Pro	Val	Ile	Ser	Leu	Tyr	Leu	Met	Gly			
	275					280						285						
Glu	Val	Thr	Asn	Gln	Ser	Phe	Arg	Ile	Thr	Ile	Leu	Pro	Gln	Gln	Tyr			
	290					295					300							
Leu	Arg	Pro	Val	Glu	Asp	Val	Ala	Thr	Ser	Gln	Asp	Asp	Cys	Tyr	Lys			
305					310					315					320			
Phe	Ala	Ile	Ser	Gln	Ser	Ser	Thr	Gly	Thr	Val	Met	Gly	Ala	Val	Ile			
			325					330					335					
Met	Glu	Gly	Phe	Tyr	Val	Val	Phe	Asp	Arg	Ala	Arg	Lys	Arg	Ile	Gly			

340 345 350  
 Phe Ala Val Ser Ala Cys His Val His  
 355 360

<210> 76  
 <211> 63  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(63)  
 <223> n = A,T,C or G

<400> 76  
 garacngayg argarccnga rgarccnggn mgnmgnggnw snttygtnga ratggtn gay 60  
 aay 63

<210> 77  
 <211> 21  
 <212> PRT  
 <213> Homo sapiens

<400> 77  
 Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val  
 1 5 10 15  
 Glu Met Val Asp Asn  
 20

<210> 78  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Peptide inhibitor P3-P4' XD-V

<221> MOD\_RES  
 <222> 3  
 <223> Xaa is hydroxyethylene or statine

<400> 78  
 Val Met Xaa Val Ala Glu Phe  
 1 5

<210> 79  
 <211> 11  
 <212> PRT  
 <213> Homo sapiens

<400> 79  
 Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val  
 1 5 10

<210> 80  
 <211> 419  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> nucleotide insert in vector pCF

<400> 80  
 ctggttgggct cgcggttgag gacaaactct tcgcggtcct tccagtactc ttggatcgga 60  
 aaccgcgcgg cctccgaacg gtactccgcc accgagggac ctgagcgagt ccgcacgcac 120  
 cggatcgga aacctctcga ctggttgggt gagtactccc tctcaaaagc gggcatgact 180  
 tctgcgctaa gattgtcagt ttccaaaaac gaggaggatt tgatattcac ctggcccgcg 240  
 gtgatgcctt tgaggggtggc cgcgtccatc tggtcagaaa agacaatctt tttgttgtca 300  
 agcttgagggt gtggcaggct tgagatctgg ccatacactt gaggagacaat gacatccact 360  
 ttgcctttct ctccacagggt gtccactccc aggtccaact gcaggtcgac tctagaccc 419

<210> 81  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Peptide inhibitor P4-P4' XD-V  
 <221> MOD\_RES  
 <222> 4  
 <223> Xaa is hydroxyethylene or statine

<400> 81  
 Glu Val Met Xaa Val Ala Glu Phe  
 1 5

<210> 82  
 <211> 9  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> APP fragment P5-P4' wt

<400> 82  
 Ser Glu Val Lys Met Asp Ala Glu Phe  
 1 5

<210> 83  
 <211> 9  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> APP fragment P5-P4'wt

<400> 83  
 Ser Glu Val Asn Leu Asp Ala Glu Phe  
 1 5

<210> 84  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> APP fragment

<400> 84  
 Ser Glu Val Lys Leu Asp Ala Glu Phe  
 1 5

<210> 85  
<211> 9  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<223> APP fragment  
  
<400> 85  
Ser Glu Val Lys Phe Asp Ala Glu Phe  
1 5  
  
<210> 86  
<211> 9  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<223> APP fragment  
  
<400> 86  
Ser Glu Val Asn Phe Asp Ala Glu Phe  
1 5  
  
<210> 87  
<211> 9  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<223> APP fragment  
  
<400> 87  
Ser Glu Val Lys Met Ala Ala Glu Phe  
1 5  
  
<210> 88  
<211> 9  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<223> APP fragment  
  
<400> 88  
Ser Glu Val Asn Leu Ala Ala Glu Phe  
1 5  
  
<210> 89  
<211> 9  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<223> APP fragment  
  
<400> 89  
Ser Glu Val Lys Leu Ala Ala Glu Phe  
1 5

<210> 90  
<211> 9  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<223> APP fragment  
  
<400> 90  
Ser Glu Val Lys Met Leu Ala Glu Phe  
1 5  
  
<210> 91  
<211> 9  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<223> APP fragment  
  
<400> 91  
Ser Glu Val Asn Leu Leu Ala Glu Phe  
1 5  
  
<210> 92  
<211> 9  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<223> APP fragment  
  
<400> 92  
Ser Glu Val Lys Leu Leu Ala Glu Phe  
1 5  
  
<210> 93  
<211> 9  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<223> APP fragment  
  
<400> 93  
Ser Glu Val Lys Phe Ala Ala Glu Phe  
1 5  
  
<210> 94  
<211> 9  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<223> APP fragment  
  
<400> 94  
Ser Glu Val Asn Phe Ala Ala Glu Phe  
1 5  
  
<210> 95

<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> APP fragment

<400> 95  
Ser Glu Val Lys Phe Leu Ala Glu Phe  
1 5

<210> 96  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> APP fragment

<400> 96  
Ser Glu Val Asn Phe Leu Ala Glu Phe  
1 5

<210> 97  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> APP-derived fragment P10-P4'(D-V)

<400> 97  
Lys Thr Glu Glu Ile Ser Glu Val Asn Leu Val Ala Glu Phe  
1 5 10

<210> 98  
<211> 35  
<212> DNA  
<213> Homo sapiens

<400> 98  
cccgaagagc ccggccggag gggcagcttt gtcga

35

<210> 99  
<211> 11  
<212> PRT  
<213> Homo sapiens

<400> 99  
Glu Thr Asp Glu Glu Pro Glu Glu Pro Gly Arg  
1 5 10

<210> 100  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Recombinant 293T cells

<400> 100

Thr Gln His Gly Ile Arg Leu Pro Leu Arg  
1 5 10

<210> 101

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant 293T cells

<400> 101

Met Val Asp Asn Leu Arg Gly Lys Ser  
1 5

<210> 102

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant CosA2 cells

<400> 102

Gly Ser Phe Val Glu Met Val Asp Asn Leu  
1 5 10

<210> 103

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> APP substrate fragment:WT Sequence

<400> 103

Val Lys Met Asp  
1

<210> 104

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> APP substrate fragment:Swedish Sequence

<400> 104

Val Asn Leu Asp  
1